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OM nucleic - nucleic search, using sw model

Run on: October 9, 2004, 22:32:20 ; Search time 13960 Seconds
            (without alignments)
            6951.179 Million cell updates/sec

Title: US-09-940-921B-1
Perfect score: 2052
Sequence: 1 atggataagtacgatgat.......cagtgtcatcctgatgtga 2052

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : GenEmbl:*
  1: gb_ba:*
  2: gb_htg:*
  3: gb_in:*
  4: gb_om:*
  5: gb_ov:*
  6: gb_pat:*
  7: gb_ph:*
  8: gb_pl:*
  9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2052	100.0	2052	6	AX394703	AX394703 Sequence
2	2052	100.0	2240	6	AX394707	AX394707 Sequence
3	1967	95.9	2949	6	BC063885	BC063885 Homo sapi
4	1868	91.0	1965	6	AX394705	AX394705 Sequence
5	1654	80.6	2370	6	AR269117	AR269117 Sequence
6	1654	80.6	2370	6	AR487609	AR487609 Sequence
7	1469.6	71.6	1947	6	AX166554	AX166554 Sequence
8	1359.8	66.3	1896	6	AX659636	AX659636 Sequence
9	1359.8	66.3	1918	6	AX659639	AX659639 Sequence
10	797.2	38.8	1884	6	CQ732078	CQ732078 Sequence
11	788.8	38.4	3635	6	CQ843384	CQ843384 Sequence
12	788.8	38.4	3635	9	AK126330	AK126330 Homo sapi
13	602	29.3	1632	6	AX803389	AX803389 Sequence
14	595.4	29.0	2281	10	BC053516	BC053516 Mus muscu
15	368	17.9	1745	9	BC068201	BC068201 Homo sapi
16	368	17.9	3645	6	AX224471	AX224471 Sequence
17	368	17.9	3729	6	AX658011	AX658011 Sequence
18	368	17.9	5426	6	AX224518	AX224518 Sequence
19	368	17.9	5448	6	AR338755	AR338755 Sequence
20	368	17.9	368	9	AB067488	AB067488 Homo sapi
21	368	17.9	5508	6	AX658014	AX658014 Sequence
22	368	17.9	5511	9	HSMB00531	AL050385 Homo sapi
23	368	17.9	5532	6	AR338754	AR338754 Sequence
24	352	17.2	4263	6	AR223879	AR223879 Sequence
25	352	17.2	5479	10	S45828	S45828 nekl=serine
26	352	17.2	958	10	AK173292	AK173292 Mus muscu
27	286	13.9	958	5	CR386196	CR386196 Gallus ga
28	255.2	12.4	2369	5	BC075119	BC075119 Xenopus t
29	253.8	12.4	876	6	AX868027	AX868027 Sequence
30	253.8	12.4	876	6	BD148089	BD148089 Primer fo
31	253.8	12.4	2975	6	AX658016	AX658016 Sequence
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33	253.8	12.4	2975	6	BD159723	BD159723 Primer fo
34	253.8	12.4	2975	9	AK027580	AK027580 Homo sapi
35	253.2	12.3	1578	6	AX657957	AX657957 Sequence
36	252.8	12.3	1581	6	AX657962	AX657962 Sequence
37	252.8	12.3	2110	6	AX504240	AX504240 Sequence
38	252.8	12.3	2134	9	BC019916	BC019916 Homo sapi
39	252.8	12.3	3255	9	AK131359	AK131359 Homo sapi
40	252	12.3	1997	10	AF093416	AF093416 Mus muscu
41	252	12.3	2025	10	AF099066	AF099066 Mus muscu
42	251.2	12.2	1610	9	AB072828	AB072828 Homo sapi
43	251.2	12.2	2364	6	AX405633	AX405633 Sequence
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45	248.8	12.1	2039	10	BC05411	BC05411 Mus muscu

ALIGNMENTS

RESULT 1
AX394703
LOCUS   AX394703   2052 bp   DNA   linear   PAT 18-MAY-2002
DEFINITION Sequence 1 from Patent WO0218555.
ACCESSION   AX394703
VERSION   AX394703.1 GI:21065806
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Friddle,C.J., Hilbun,E., Nepomnichy,B. and Hu,Y.
  TITLE   Human kinase proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 0218555-A 1 07-MAR-2002;
            Lexicon Genetics Incorporated (US)
FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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ORIGIN

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Best Local Similarity   100.0%; Pred. No. 0;
Matches 2052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCAAGTGCCTTCGGCAAAGCATACTTA 60
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Db   1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCAAGTGCCTTCGGCAAAGCATACTTA 60

Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCTAAAGGGAAATCAGATAGCAAGCACGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG 120

Qy   121 CCCATACAAGAAAAAGAAGCTTCAAAGAAGTGATTCTTCTGGAAAGATGAAACAT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCCATACAAGAAAAAGAAGCTTCAAAGAAGTGATTCTTCTGGAAAGATGAAACAT 180

Qy   181 CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAGAGATGGCAGGCTGTTTATTGTAATG 240
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Db   181 CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAGAGATGGCAGGCTGTTTATTGTAATG 240

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Qy   241  GAATATTGTGATGGAGGGATCTCATGAAAGGATCAATAGACAACGGGGTCGTGTTATTT  300
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Db   241  GAATATTGTGATGGAGGGATCTCATGAAAGGATCAATAGACAACGGGGTGTGTGTTATTT  300

Qy   301  AGTGAAGATCAGATCCTCGGTTGGTTGTTACAGATTTCTCTAGGACTAAAACATATTCAT  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AGTGAAGATCAGATCCTCGGTTGGTTGTTACAGATTTCTCTAGGACTAAAACATATTCAT  360

Qy   361  GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA   420
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Db   361  GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA   420

Qy   421  ATGGTGCAAAGCTTGGGACTTGGTATAGACAAGAGTCCTGAATAATTCCATGGAACTT   480
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Db   421  ATGGTGGCAAAGCTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT   480

Qy   481  GCTCGAACTTGTATTGGAACACCTTACTACCTTGTCCCCAGAGATCTCGTCAGAATAAACCC  540
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Db   481  GCTCGAACTTGTATTGGAACACCTTACTACCTTGTCCCCAGAGATCTCGTCAGAATAAACCC  540

Qy   541  TACAACAATAAAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT  600
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Db   541  TACAACAATAAAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT  600

Qy   601  AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTCAAGATTTGTCAAGACAT   660
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Db   601  AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTCAAGATTTGTCAAGACAT   660

Qy   661  TTTGCCCCAATATCTCCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT  720
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Db   661  TTTGCCCCAATATCTCCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT  720

Qy   721  CAAGTATCTCCTCGAGACCGACCATCCAATAAATTCCATTTGAAAAGGCCCTTTTTAGAG  780
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Db   721  CAAGTATCTCCTCGAGACCGACCATCCAATAAATTCCATTTGAAAAGGCCCTTTTTAGAG  780

Qy   781  AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT  840
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Db   781  AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT  840

Qy   841  ATATGCAGAGCAGGAGCGCCAGTTCTTCGACATGCTGGACATGCTTCTGGGAAGTGTAAA  900
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Db   841  ATATGCAGAGCAGGAGCGCCAGTTCTTCGACATGCTGGACATGCTTCTGGGAAGTGTAAA  900

Qy   901  ATACAAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATATCTGTGCCAATT   960
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Db   901  ATACAAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATATCTGTGCCAATT   960

Qy   961  AAAAGGAATGCTATATTGCATAGAAAATGAATGAATGAAATGAGAGCCTGAGCCCCAGAGGCC  1020
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Db   961  AAAAGGAATGCTATATTGCATAGAAAATGAATGAATGAAATGAGAGCCTGAGCCCCAGAGGCC  1020

Qy  1021  AGATCTATAAAAATGATAGAAAGACCCAAAATTGCTCGTGTCGTGTGGACATTATGATTAT  1080
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Db  1021  AGATCTATAAAAATGATAGAAAGACCCAAAATTGCTCGTGTCGTGTGGACATTATGATTAT  1080

Qy  1081  TATTATGCTCAACTTGATATGTGAGGAGGAGCCCACAAACCAAGTTATCACCCTATT  1140
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Db  1081  TATTATGCTCAACTTGATATGTGAGGAGGAGCCCACAAACCAAGTTATCACCCTATT  1140

Qy  1141  CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAAACAGGCATGGTCCATCCCCA  1200
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Db  1141  CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAAACAGGCATGGTCCATCCCCA  1200

Qy  1201  AGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTTGAAGTCAACATATAAGTTGAAA   1260
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Db  1201  AGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTTGAAGTCAACATATAAGTTGAAA   1260

Qy  1261  GTGGAGAAGCAATTGGGTCTTCGTCTCCATCTTCGCGAGCCAAATTACAACCAGAGACAA  1320
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Qy  1321  GAGCTAAGAGTAATGAGAGAGAGCCTAGATTCCAGGAGTGCCATTTAGGAAAAACGAA  1380
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Db  1321  GAGCTAAGAGTAATGAGAGAGAGCCTAGATTCCAGGAGTGCCATTTAGGAAAAAACGAA  1380

Qy  1381  ATGAAGGAACAGGAATATTGGAAGCAGTTAGAGAGAAATACGCCAACAGTACCACCAATGAC  1440
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Db  1381  ATGAAGGAACAGGAATATTGGAAGCAGTTAGAGAGAAATACGCCAACAGTACCACCAATGAC  1440

Qy  1441  ATGAAAGAAATTAGAAGAGATGGGAGAACCAGAGAGAACTCAAAAATAAGTCAT  1500
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Db  1441  ATGAAAGAAATTAGAAGAGATGGGAGAACCAGAGAGAACTCAAAAATAAGTCAT  1500

Qy  1501  AAAACCTATTGGTGAAGAAGAGTAACCTGCCTGTCATCAAGATGCATCTGAGGGAGAA  1560
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Db  1501  AAAACCTATTTGGTGAAGAAGAGTAACCTGCCTGTCCATCAAGATGCATCTGAGGGAGAA  1560

Qy  1561  GCACCTGTGCAGGACATTGAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGAA  1620
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Db  1561  GCACCTGTGCAGGACATTGAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGAA  1620

Qy  1621  AGTAAAAATCCAGAACAGAAATATAAAAGCTAAGAGAGGGGTAAAATTTGAAATTAATTTA  1680
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Db  1621  AGTAAAAATCCAGAACAGAAATATAAAAGCTAAGAGAGGGGTAAAATTTGAAATTAATTTA  1680

Qy  1681  GACAAATGTATTTCTGATGAAAACATCCCCAAGAGGAAGAGGCAATGATATACCAAAT  1740
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Db  1681  GACAAATGTATTTCTGATGAAAACATCCCCAAGAGGAAGAGGCAATGATATACCAAAT  1740

Qy  1741  GAAACTTTGACCTTTGAGGATGGCATGAAGACAAAGCATTGAAAAACTTCACTCGCCCAGAGCAGGTTTTCCACG  1800
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Db  1741  GAAACTTTGACCTTTGAGGATGGCATGAAGACAAAGCATTGAAAAACTTCACTCGCCCAGAGCAGGTTTTCCACG  1800

Qy  1801  GGAGTATATCAGACAAAGCATTTGAAAAGAGCATTTGAAAAACAGCAGTGGGATGGGAGGCGCCTCAGACTCTG  1860
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Db  1801  GGAGTATATCAGACAAAGCATTTGAAAAGAGCATTTGAAAAACAGCAGTGGGATGGGAGGCGCCTCAGACTCTG  1860

Qy  1861  CAGACTGTAGCTGCGTGTGGGAAACAGGAGGCAGTGGGATGGGATGGGAGCCCCAGGGGCCGTACAGCCCAGTGCTC  1920
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Db  1861  CAGACTGTAGCTGCGTGTGGGAAACAGGAGGCAGTGGGATGGGATGGGAGCCCCAGGGGCCGTACAGCCCAGTGCTC  1920

Qy  1921  CTGCAGGATGATGGCGCAGTGGCCGCGACATCACCTCCCACGGGAAGAGACCAAGGACCCGTACAGCCCAGTGCTC  1980
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Db  1921  CTGCAGGATGATGGCGCAGTGGCCGCGACATCACCTCCCACGGGAAGAGACCAAGGACCCGTACAGCCCAGTGCTC  1980

Qy  1981  TCTGTGCTTAGCGTCAGTCGTCTGTGGGAAACAGGAGGCAGGAAGGAAGAGAAGAGACCCGTACAGCCCCAGTGCTC  2040
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Db  1981  TCTGTGCTTAGCGTCAGTCGTCTGTGGGAAACAGGAGGCAGGAAGGAAGAGAAGAGACCCGTACAGCCCCAGTGCTC  2040

Qy  2041  ATCCTGATGTGA  2052
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Db  2041  ATCCTGATGTGA  2052
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RESULT 2
AX394707

LOCUS   AX394707   2240 bp   DNA   linear   PAT 18-MAY-2002
DEFINITION Sequence 5 from Patent WO0218555.
ACCESSION   AX394707
VERSION   AX394707.1 GI:21065808
KEYWORDS
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Friddle,C.J., Hilbun,B., Nepomnichy,B. and Hu,Y.
  TITLE   Human kinase proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 0218555-A 5 07-MAR-2002;
            Lexicon Genetics Incorporated (US)
FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
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ORIGIN   /db_xref="taxon:9606"

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Query Match     100.0%;  Score 2052;  DB 6;  Length 2240;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 2052;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy      1  ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGGCAAGGTGCCTTGGGAAAGCATACTTA   60
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Db    105  ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGGCAAGGTGCCTTGGGAAAGCATACTTA  164

Qy     61  GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG    120
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Db    165  GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG   224

Qy    121  CCCATACAAGAAAAAGAGAAGCTTCAAGAGGGATCTTCTCAAATTCATTCAAGAGAATGG   180
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Db    225  CCCATACAAGAAAAAGAGAAGCTTCAAGAGGGATCTTCTCAAATTCATTCAAGAGAATGG   284

Qy    181  GAATATTGTGATGGAGGGGATCCTCGTTGGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT  240
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Db    285  GAATATTGTGATGGAGGGGATCCTCGTTGGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT  344

Qy    241  AGTGAAGATCAGATCTCCGTTGGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT   300
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Db    345  AGTGAAGATCAGATCTCCGTTGGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT  404

Qy    301  GACAGGGAAGATATTACACAGGGACATAAATAAAGCCAGGAGAACCAGGAGAACGGA  360
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Db    405  GACAGGGAAGATATTACACAGGGACATAAATAAAGCCAGGAGAACCAGGAGAACGGA  464

Qy    361  ATGGTGGCAAAGCTTGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  420
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Db    465  ATGGTGGCAAAGCTTGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  524

Qy    421  GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCAGAGATCGTCAGAATAAACCC  480
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Db    525  GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCAGAGATCGTCAGAATAAACCC  584

Qy    481  TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT  540
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Db    585  TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT  644

Qy    541  AAACATCCTTTGAGGGTAACACTTACAGCAGCTGGTTCTCAAGATTTGTCAAGCACAT   600
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Db    645  AAACATCCTTTGAGGGTAACACTTACAGCAGCTGGTTCTCAAGATTTGTCAAGCACAT  704

Qy    601  TTTGCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTGATATCTCAGCTCTTT  660
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Db    705  TTTGCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTGATATCTCAGCTCTTT  764

Qy    661  CAAGTATCTCCTCGAGACCGACCACCATCCATAAATTCCATTTTGAAAAGGCCCTTTTTTAGAG  720
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Db    765  CAAGTATCTCCTCGAGACCGACCACCATCCATAAATTCCATTTTGAAAAGGCCCTTTTTTAGAG  824

Qy    721  AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT   780
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Db    825  AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT  884

Qy    781  ATATGCAGAGCAGGAGCGCCGAGCTTCTCGACATGCTGGAGGTAACGTTGGTCCAGAGTGTAAA   840
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Db    885  ATATGCAGAGCAGGAGCGCCGAGCTTCTCGACATGCTGGAGGTAACGTTGGTCCAGAGTGTAAA  944

Qy    841  ATACAAAAAGTGAGATTCGATTTCAGGGAAAGTGCCAAGATCAAGGATATCTGTGCCAATT   900
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Db    945  ATACAAAAAGTGAGATTCGATTTCAGGGAAAGTGCCAAGATCAAGGATATCTGTGCCAATT  1004

Qy    901  AAAAGGAATGCTATATTGCATAGAAATGAATGGACACCACCAGCTGGAGCCCAGAAGGCC   960
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Db   1005  AAAAGGAATGCTATATTGCATAGAAATGAATGGACACCACCAGCTGGAGCCCAGAAGGCC  1064

Qy    961  AAAAGGAATGCTATATTGCATAGAAATGAATGGACACCACCAGCTGGAGCCCAGAAGGCC  1020
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Db   1065  AAAAGGAATGCTATATTGCATAGAAATGAATGGACACCACCAGCTGGAGCCCAGAAGGCC  1124

Qy   1021  AGATCTATAAAAATGAATAGAAAGACCCAAAAATTGCTGCTTGTCTGTGGGACATTATGATTAT  1080
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Db   1125  AGATCTATAAAAATGAATAGAAAGACCCAAAAATTGCTGCTTGTCTGTGGGACATTATGATTAT  1184

Qy   1081  TATTATGCTCAACTTGATATGTCTGAGGAGGAGCCCACAAACCAAGTTATCACCCTATT  1140
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Db   1185  TATTATGCTCAACTTGATATGTCTGAGGAGGAGCCCACAAACCAAGTTATCACCCTATT  1244

Qy   1141  CCTCAAGAAAAATACTGGAGTTGAGGATTACGGTCAGAGAAACGAGGCGATGGTCCATCCCCA  1200
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Db   1245  CCTCAAGAAAAATACTGGAGTTGAGGATTACGGTCAGAGAAACGAGGCGATGGTCCATCCCCA  1304

Qy   1201  AGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACATATAAGTTGAAA  1260
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Db   1305  AGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACATATAAGTTGAAA  1364

Qy   1261  GTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA  1320
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Db   1365  GTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA  1424

Qy   1321  GAGCTAAGAGTAATGGAGAAGAGCCTAGATTCCAGGAAGCTGCCATTGGAGAAAACGAA  1380
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Db   1425  GAGCTAAGAGTAATGGAGAAGAGCCTAGATTCCAGGAAGCTGCCATTGGAGAAAACGAA  1484

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Qy   1621  AGTAAAAATCCAGAACAGAAATATAAAGCTAAGAAGGGGTAAAATTTGAAATTAATTTA  1680
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Db   1785  GACAAATGTATTCTGATGAAAACATCCTCCAAGAGGAAGAGCAATGCAATGGATATACCAAAT  1844

Qy   1741  GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGTGTAAAGGAGCAT  1800
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Db   1905  GGGAGATTATACAGACAAAGCATTTGAAAAACTTCACTGCCCGAAGCAGGGTTTTCACG  1964

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Qy   1921  CTGCAGATGATGGCAGTGCAGTGCCGACATCACCTCCACCTGCCCACCGGCCTGACAGTGAG  1980
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Db   2025  CTGCAGATGATGGCAGTGCAGTGCCGACATCACCTCCACCTGCCCACCGGCCTGACAGTGAG  2084

Qy   1981  TCTGTGCTTAGCGTCAGTCGTCAGGAAGAGACCCAAGGAGACCCGTACAGCCCAGTGCTC  2040
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Qy   2041  ATCCTGATGTGA  2052
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Db   2145  ATCCTGATGTGA  2156
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```
RESULT 3
BC063885
LOCUS       BC063885               2949 bp    mRNA    linear   PRI 06-JAN-2004
DEFINITION  Homo sapiens similar to Serine/threonine-protein kinase Nek1
            (NimA-related protein kinase 1), mRNA (cDNA clone MGC:75495
            IMAGE:30383658), complete cds.
ACCESSION   BC063885
VERSION     BC063885.1  GI:39645656
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2949)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 2949)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-DEC-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 141 Row: m Column: 21
            This clone was selected for full length sequencing because it
            passed the following selection criteria: GenomeScan gene
            prediction, Similarity but not identity to protein.
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                     phosphorylation of specific residues in the activation
                     segment of the catalytic domain, sometimes combined with
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Best Local Similarity    96.5%;  Pred. No. 0;
Matches 2052;  Conservative    0;  Mismatches    0;  Indels   75;  Gaps    1;

Qy          1 ATGGATAAGTACGATGTGATTAAGGCCATCGGACCAAGGTGCCTTCGGGAAAGCATACTTA 60
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Qy        121 CCCATACAAGAAAGAAGAAGCTTCAAGAAAGAAGTGATTCTTCTGGAAAAGATGAAACAT 180
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Qy   1501  AAAACCTATTTGGTGAAGAAGAGTAACCTGCCTGCCATCAAGATGCATCTGAGGGAGAA  1560
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Qy   1561  GCACCTGTG-----------------------------------------------  1569
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Db   1701  GCACCTGTGCAGATGGAATTTGCGTCTGTTGTGCCGAGGCTGGAGTGCAATGGCACGATCT  1760

Qy   1570  ----------------CAGGACATTGAAAAAGACTTGAAACAAATGAGGCTT  1605
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Db   1761  TGGCTCACCGCAACCTCCGCCTCCCAGGACATTGAAAAAGACTTGAAACAAATGAGGCTT  1820

Qy   1606  CAGAACACAAAGGAAAGTAAAAATCCAGAACAGAATATAAAGTAAGTAAGGGGTAAAA  1665
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Db   1821  CAGAACACAAAGGAAAGTAAAAATCCAGAACAGAATATAAAGTAAGTAAGGGGTAAAA  1880

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Db   2121  GCGCCTCAGACTCTGCTGCGAGATGATGGCCAGTGGCCGACATCACCTCCCACG  2180

Qy   1966  GGGCCTGACAGTGAGTCTGTCTGCTTAGCGTCAGGCGTCAGGAAGGGAAGACCAAGGACCCG  2025
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Db   2241  TACAGCCCCAGTGCTCATCCTGATGTGA  2267
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RESULT 4
AX394705

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LOCUS       AX394705                   1965 bp     DNA         linear   PAT 18-MAY-2002
DEFINITION  Sequence 3 from Patent WO0218555.
ACCESSION   AX394705
VERSION     AX394705.1   GI:21065807
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Friddle,C.J., Hilbun,E., Nepomnichy,B. and Hu,Y.
  TITLE     Human kinase proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 0218555-A 3 07-MAR-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match   91.0%; Score 1868; DB 6; Length 1965;
Best Local Similarity   95.8%; Pred. No. 0;
Matches 1965; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

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Left column alignment blocks:

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Qy   1441  ATGAAAAGAATTAGAAAGAAGAGATGGGAAGAGAACCAGAGGAGAACTCAAAAATAAGTCAT  1500
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Db  1081 TATTATGCTCAACTTGATATGCTGAGGAGGAGAGCCCACAAACCAAGTTATCACCCTATT 1140
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Qy  1141 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCATGGTCCATCCCCA 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCATGGTCCATCCCCA 1200

Qy  1201 AGTCAATGGCCTGCTGAGTACCTTCAGAGAAAATTTGAAGTCAACAATATAAGTGTGAAA 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 AGTCAATGGCCTGCTGAGTACCTTCAGAGAAAATTTGAAGTCAACAATATAAGTGTGAAA 1260

Qy  1261 GTGGAGAAGCAATTGGGTCTTCGTCCCATCTTCTGCCGAGCCAATTACAACCAGAGACAA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GTGGAGAAGCAATTGGGTCTTCGTCCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA 1320

Qy  1321 GAGCTAAGAGAGTAATGGAGAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAAAAAACGAA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 GAGCTAAGAGAGTAATGGAGAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAAAAAACGAA 1380

Qy  1381 ATGAAGGAACAAGGAATATTGAAGCAATGTTAGAGGAAATACCCAACAGTACCACAATGAC 1440
         ||||||||||
Db  1381 ATGAAGGAAC---------------------------------------------------- 1390

Qy  1441 ATGAAAGAAATTAGAAAAGAATGGGGAGAGAACCAGAGAGAACTCAAAAATAAGTCAT 1500
         ||||||||||||||||||||||||||||||||     --AGGAGAACTCAAAAATAAGTCAT
Db  1391 ---------------------------------AGGAGAACTCAAAAATAAGTCAT 1413

Qy  1501 AAAACCTATTTGGTGAGAGAGTAACCTGCCGTGTCCATCAGATGCATCTGAGGGAGAA 1560
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Db  1414 AAAACCTATTTGGTGAGAGAGTAACCTGCCGTGTCCATCAAGATGCATCTGAGGGAGAA 1473

Qy  1561 GCACCTGTGCAGGACATTGAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGAA 1620
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Db  1474 GCACCTGTGCAGGACATTGAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGAA 1533

Qy  1621 AGTAAAAATCCAGAACAGAAATATAAAGCTAAGAGGGGTAAAATTTGAAATTAATTTA 1680
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Db  1534 AGTAAAAATCCAGAACAGAAATATAAAGCTAAGAGGGGTAAAATTTGAAATTAATTTA 1593

Qy  1681 GACAAATGTATTTCTGATGAAAACATCCTCAAGAGAGGCAATGGATATACCAAAT 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1594 GACAAATGTATTTCTGATGAAAACATCCTCAAGAGAGGCAATGGATATACCAAAT 1653

Qy  1741 GAAACTTTGACCTTTGAGGATGGCATGAGTTTAAGGAATGTAAAGGAGCAT 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1654 GAAACTTTGACCTTTGAGGATGGCATGAGTTTAAGGAATGTAAAGGAGCAT 1713

Qy  1801 GGGAGATTATACAGACAAAAGCATTTGAAAAACTTCACTGCCCAGAGCAGGGTTTCCACG 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1714 GGAGATTATACAGACAAAAGCATTTGAAAAACTTCACTGCCCAGAGCAGGGTTTCCACG 1773

Qy  1861 CAGACTGTAGCTGCTGTGGGAAACAGAGCAGTGGGATGGAGGAGCGCCTCAGACTCTG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1774 CAGACTGTAGCTGCTGTGGGAAACAGAGCAGTGGGATGGAGGAGCGCCTCAGACTCTG 1833

Qy  1921 CTGCAGATGATGGCCAGTGGCCGACATCACCTGCCCACCTGCCCACGGGGCCTGACAGTGAG 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1834 CTGCAGATGATGGCCAGTGGCCGACATCACCTGCCCACCTGCCCACGGGGCCTGACAGTGAG 1893

Qy  1981 TCTGTGCTTAGCGTCAGTGCTCGTCAGGAAGGAAGACCCGTACAGCCCAGTGCTC 2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1894 TCTGTGCTTAGCGTCAGTGCTCGTCAGGAAGGAAGACCCGTACAGCCCAGTGCTC 1953

Qy  2041 ATCCTGATGTGA 2052
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Db  1954 ATCCTGATGTGA 1965
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RESULT 5
AR269117

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LOCUS       AR269117               2370 bp    DNA         linear    PAT 10-APR-2003
DEFINITION  Sequence 1 from patent US 6500655.
ACCESSION   AR269117
VERSION     AR269117.1  GI:29699967
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Db    1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCAAGTGCCTTCGGCAAAGCATACTTA 60
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Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTCATAAAGAGATCAATTTGAAAAGAATG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTCATAAAGAGATCAATTTGAAAAGAATG 120

Qy  121 CCCATACAAGAAAAAGAGAGCTTCAAAGAAGAGTGATTCTTCTGGAAAAGATGAAACAT 180
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Db  121 CCCATACAAGAAAAAGAGAGCTTCAAAGAAGAGTGATTCTTCTGGAAAAGATGAAACAT 180

Qy  181 CCCAACATTGTAGCCTTCATTCAGCAGGCTGTTTATTGTAATG 240
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Db  181 CCCAACATTGTAGCCTTCATTCAGCAGGCTGTTTATTGTAATG 240

Qy  241 GAATATTGTGATGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATTT 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GAATATTGTGATGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATTT 300

Qy  301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360

Qy  361 GACAGGAAGAGATATTACACAGGGACATAAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
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Db  361 GACAGGAAGAGATATTACACAGGGACATAAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420

Qy  421 ATGGTGGCAAGCTTGGGACTTTGGTATAGCAAGTCCTGAATAATTCCATGGAACTT 480
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Qy  481 GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCC 540
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Qy  541 TACAACAATAAAACGATATTTGGTCTTCTGGCTGTCTTATATGAGCTCTGCACACTT 600
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Db  541 TACAACAATAAAACGATATTTGGTCTTCTGGCTGTCTTATATGAGCTCTGCACACTT 600

Qy  601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTTGTCAAGCACAT 660
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Db  601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTTGTCAAGCACAT 660

Qy  661 TTTGCCCCAATATCTCCGGGGTTTCTTCGTGAGCTCCATTCCTTGATATCCCAGCTCTTT 720
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Db  661 TTTGCCCCAATATCTCCGGGGTTTCTTCGTGAGCTCCATTCCTTGATATCCCAGCTCTTT 720

Qy  721 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAAGGCCCATTTGTGCCAATT 780
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Db  721 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAAGGCCCATTTGTGCCAATT 780

Qy  781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGGAGAATTCAGTGCATGCTT 840
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Db  781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGGAGAATTCAGTGCATGCTT 840

Qy  841 ATATGCAGAGCAGGAGGCGCTATATTGCATAGAAATGATGAGCCCAGAAGGCC 900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 ATATGCAGAGCAGGAGGCGCTATATTGCATAGAAATGATGAGCCCAGAAGGCC 900

Qy  901 ATACAAAAAGTGAGATTGCCCACCAAGAGTCGTGTGCTCTCGTCTGTGCTCTGTGCTGCCAATT 960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 ATACAAAAAGTGAGATTGCCCACCAAGAGTCGTGTGCTCTCGTCTGTGCTCTGTGCTGCCAATT 960

Qy  961 AAAAGGAATGCTATATTGATAGAAAAGAGCCCAAAATTGCTGTGCTCTGTGCTGGACATTATGATTAT 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 AAAAGGAATGCTATATTGATAGAAAAGAGCCCAAAATTGCTGTGCTCTGTGCTGGACATTATGATTAT 1020

Qy 1021 AGATCCTATAAAAATGATAGAAAAGACCCAAAATTGCTGTGCTCTGTGCTGGACATTATCACCCTATT 1080
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 AGATCCTATAAAAATGATAGAAAAGACCCAAAATTGCTGTGCTCTGTGCTGGACATTATCACCCTATT 1080

Qy 1081 TATTATGCTCAACTTGATATGCTGAGGAGGAGAGCCCACAAACCAAGTTATCACCCTATT 1140
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KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 2370)
AUTHORS     Webster,M., Yan,C., Di Francesco,V. and Beasley,E.
TITLE       Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
JOURNAL     Patent: US 6500656-A 1 31-DEC-2002;
FEATURES    Location/Qualifiers
source      1..2370
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN

Query Match   80.6%;   Score 1654;   DB 6;   Length 2370;
Best Local Similarity  94.5%;
Matches 1763;   Conservative 0;   Mismatches 10;   Indels 93;   Gaps 1;

Qy    1 ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAAGCATACTTA   60
         |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   12 ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAAGCATACTTA   71

Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCTATAAAAGAGATCAATTTGAAAAGAGATG  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   72 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCTATAAAAGAGATCAATTTGAAAAGAGATG  131

Qy  121 CCCATACAAGAAAAGAAGCTTCAAAGAGAAGAGTGATTCTTCTGAAAAAGATGAAACAT  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  132 CCCATACAAGAAAAGAAGCTTCAAAGAGAAGAGTGATTCTTCTGAAAAAGATGAAACAT  191

Qy  181 CCCAACATTGTGAGCCTTCTCAATTCATTTCAAGAAGAATGGCAGGCTGTTTATTGTAATG  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  192 CCCAACATTGTGAGCCTTCTCAATTCATTTCAAGAAGAATGGCAGGCTGTTTATTGTAATG  251

Qy  241 GAATATTGTGATGGAGGGGATCTCATGAGAAAAGGATCAATGAAACACGGGGTGTTTATTT  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252 GAATATTGTGATGGAGGGGATCTCATGAGAAAAGGATCAATGAAACACGGGGTGTTTATTT  311

Qy  301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCCTAGGACTAAAACATATTCAT  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  312 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCCTAGGACTAAAACATATTCAT  371

Qy  361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA  420
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Db  372 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA  431

Qy  421 ATGGTGGCAAAGCTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  432 ATGGTGGCAAAGCTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  491

Qy  481 GCTCGAACTTGTATGGGAACACACTTGACCTCCGGGTTTTCTCGTGAGCTTCTGATCTCTT  540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  492 GCTCGAACTTGTATGGGAACACACTTGACCTCCGGGTTTTCTCGTGAGCTTCTGATCTCTT  551

Qy  541 TACAACAATAAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTGCACAACT  600
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Db  552 TACAACAATAAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTGCACAACT  611

Qy  601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTCCGAAGATTTGTCAAGCACAT  660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  612 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTCCGAAGATTTGTCAAGCACAT  671

Qy  661 TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTTCCATTCCTTGATATCTCAGCTCTTT  720
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Db  672 TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTTCCATTCCTTGATATCTCAGCTCTTT  731

Qy  721 CAAGTATCTCCTGGAGACCGACCATCCAATAAATCCATAAATTCCATTTTGAAAAGGCCCTTTTTTGAG  780
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Db  732 CAAGTATCTCCTGGAGACCGACCATCCAATAAATCCATAAATTCCATTTTGAAAAGGCCCTTTTTAGAG  791

Qy  781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT  840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  792 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT  851

Qy  841 ATATGCAGCAGAGCGCAGCTTCGACATGCTGGACATGCTGGGAAGGTGGTCCAGAAGTGTAAA  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  852 ATATGCAGCAGAGCGCAGCTTCGACATGCTGGACATGCTGGGAAGGTGGTCCAGAAGTGTAAA  911

Qy  901 ATACAAAAAGTGAGATTCCAGGAAAGTGCCCCAAGATCAAGGATATCTGTGCCAATT  960
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Db  912 ATACAAAAAGTGAGATTCCGGGGAAAGTGCCCCAAGATCAAGGATATCTGTGCCAATT  971

Qy  961 AAAAGGAATGCTATATTGCATAGAAATGATGAAGACCCCAGCTGGACCCAGAAGGCC  1020
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Db  972 AAAAGGAATGCTATATTGCATAGAAATGAATGAGACCACCAGCTGGACCCAGAAGGCC  1031

Qy 1021 AGATCTATAAAAATGATAGAAACCCAAAATTGCTGCTGTGTCTGTGGACATTATGATTAT  1080
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Db 1032 AGATCTATAAAAATGATAGAAACCCAAAATTGCTGCTGTGTCTGTGGACATTATGATTAT  1091

Qy 1081 TATTATGCTCAACTGATATGCTGAGGAGGAGCCCACAAACCAAGTTATCACCCTATT  1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1092 TATTATGCTCAACTGATATGCTGAGGAGGAGCCCACAAACCAAGTTATCACCCTATT  1151

Qy 1141 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAAATTTGAAGCATCAACATATAGTTGAAA  1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1152 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAAATTTGAAGCATCAACATATAGTTGAAA  1211

Qy 1201 AGTCAATGGCCTGCTGCTGAGTACCTTCAGGAGAAATTGATTCTTCTGCGAGCCAAATTACAACCAGAGACAA  1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1212 AGTCAATGGCCTGCTGCTGAGTACCTTCAGGAGAAATTGATTCTTCTGCGAGCCAAATATAACCAGAGACAA  1271

Qy 1261 GTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCGAGCCAAATTACAACCAGAGACA  1320
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Db 1272 GTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCGAGCCAAATTACAACCAGAGACA  1331

Qy 1321 GAGCTAAGAAGTAATGGAGGAATATTGGAGCAGTAGCACCTAGATTCCAGGAAAAAACGAA  1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1332 GAGCTAAGAAGTAATGGAGGAATATTGGAGCAGTAGCACCTAGATTCCAGGAAAAAACGAA  1391

Qy 1381 ATGAAGGAACAGGAATATTGGAAGCAGCAGTTAGAGGAAATACGCCAACAGTACCACAATGAC  1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1392 ATGAAGGAACAGGAATATTGGAAGCAGCAGTTAGAGGAAATACGCCAACAGTACCTCAATGAC  1451

Qy 1441 ATGAAAGAAATTAGAAGAAGATGGGAGAGAAGATGGGGAGAACTCAAAAATAAGTCAT  1500
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Db 1452 ATGAAAGAAATTAGAAGAAGATGGGAGAGAAGATGGGGAGAACCAG-------------  1488

Qy 1501 AAAACCTATTTGGTGAAGAGAGTAACCTGCCTGTCCATCAAGATGCATCTGAGGGAGAA  1560
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Db 1489 --------------------------------------------------------------  1488

Qy 1561 GCACCTGTCGCAGGACATTGAAACAAATGAGGCTTCAGAAACAAATGAGGCTTCAGAAACACAAAGGAA  1620
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Db 1489 ----------AGGACATTGAAACAAATGAGGCTTCAGAAACAAATGAGGCTTCAGAAACACAAAGGAA  1538

Qy 1621 AGTAAAATCCAGAACGAAGAAATATAAAGCTAAGAAGGGGTAAAATTTAATTTA  1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1539 AGTAAAATCCAGAACAGAAGAAATATAAAGCTAAGAAGGGGTAAAATTTAATTTA  1598

Qy 1681 GACAAATGTATTTCTGATGAAAAACATCCTCCAAGAGAGGCCAATGCAATATACCAAAT  1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1599 GACAAATGTATTTCTGATGAAAAACATCCTCCAAGAGAGGCCAATGCAATATACCAAAT  1658

Qy 1741 GAAACTTTGACCTTTGAGGATGCCATGAAGTTTAAGGAATGTGTAAAGGAGCAT  1800
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Db 1659 GAAACTTTGACCTTTGAGGATGCCATGAAGTTTAAGGAATGTGTAAAGGAGCAT  1718

Qy 1801 GGAGATTATACAGACAAAGCATTTGAAAAACTTCACTGCCCGAAGCAGGGTTTTCACG  1860
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Db 1719 GGAGATTATACAGACAAAGCATTTGAAAAACTTCACTGCCCGAAGCAGCAGCATTTACAGAA  1778

Qy 1861 CAGACT  1866
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Db 1779 CTGACT  1784
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RESULT 6
AR487609

LOCUS       AR487609        2370 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 1 from patent US 6706510.
ACCESSION   AR487609
VERSION     AR487609.1  GI:47252885
KEYWORDS    
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2370)
  AUTHORS   Webster,M., Yan,C., Di Francesco,V. and Beasley,E.
  TITLE     Isolated human kinase proteins
  JOURNAL   Patent: US 6706510-A 1 16-MAR-2004;
FEATURES             Location/Qualifiers
     source          1..2370
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                     /mol_type="genomic DNA"
ORIGIN

Query Match            80.6%;  Score 1654;  DB 6;  Length 2370;
Best Local Similarity  94.5%;
Matches 1763;  Conservative  0;  Mismatches 10;  Indels 93;  Gaps 1;

Qy     1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCACTTCGGGGAAGCATACTTA 60
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Db    12 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCACTTCGGGGAAGCATACTTA 71

Qy    61 GCTAAAGGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    72 GCTAAAGGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 131

Qy   121 CCCATACAAGAGAAAAGAAGCTTCAAAGAGAAAAGAAGTGATTCTTCTGGAAAAGATGAAACAT 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   132 CCCATACAAGAGAAAAGAAGCTTCAAAGAGAAAAGAAGTGATTCTTCTGGAAAAGATGAAACAT 191

Qy   181 CCCAACATTGTAGCCTTCTTCTTCTTCAATTCATTCAAGAGAATGCCAGGCTGTGTTATTGTAATG 240
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Db   192 CCCAACATTGTAGCCTTCTTCTTCTTCAATTCATTCAAGAGAATGCCAGGCTGTGTTATTGTAATG 251

Qy   241 GAATATTGTGATGGAGGGGATCCTCGGTTGGTTCTCGGTGTGTCAATAGACAACGGGGTGTGTATTT 300
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Db   252 GAATATTGTGATGGAGGGGATCCTCGGTTGGTTCTCGGTGTGTCAATAGACAACGGGGTGTGTATTT 311

Qy   301 AGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTTCTTGTACAGATAAAACATATTCAT 360
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Db   312 AGTCAAGATCAGATCCTCGGTTGGTTGTACAGATTTCTTGTACAGATAAAACATATTCAATGAC 371

Qy   361 GACAGGAGAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
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Db   372 GACAGGAGAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 431

Qy   421 ATGGTGCCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
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Db   432 ATGGTGCCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 491

Qy   481 GCTCGAACTTGTATTGGAACACCTTACACCTTGGTCTCCCCCAGAGATCGTCCCCAGAATAAACCC 540
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Db   492 GCTCGAACTTGTATTGGAACACCTTACACCTTGGTCTCCCCCAGAGATCGTCCCCAGAATAAACCC 551

Qy   541 TACAACAATAAACGGATATTGGTCTCTTGGCGTGTCTTATATGAGCTCTGCCACACTT 600
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Db   552 TACAACAATAAACGGATATTGGTCTCTTGGCGTGTCTTATATGAGCTCTGCCACACTT 611

Qy   601 AAACATCCTTTGAGGGTAACAACTTACAGACAGATTGTTCAAGCACAT 660
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Db   612 AAACATCCTTTGAGGGTAACAACTTACAGACAGATTGTTCAAGCACAT 671

Qy   661 TTTGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCCTCAGTCTCTTT 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   672 TTTGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCCTCAGTCTCTTT 731


Qy   721 CAAGTATCTCCTCGAGACCGACCACCATCCATTTTGAAAAGGCCCTTTTTTAGAG 780
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Db   732 CAAGTATCTCCTCGAGACCGACCACCATCCATTTTGAAAAGGCCCTTTTTTAGAG 791

Qy   781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAGATTCAGTCACATGCTT 840
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Db   792 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAGATTCAGTCACATGCTT 851

Qy   841 ATATGCAGAGCAGGAGCGCGCCAGCTTCTCGACATGCTGGGAAGGTGTCGCAGAAGTGTAA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   852 ATATGCAGAGCAGGAGCGCGCCAGCTTCTCGACATGCTGGGAAGGTGTCGCAGAAGTGTAA 911

Qy   901 ATACAAAAAGTGAGATTCAGGGAAGTGCCACCAAGATCAAGGATATCTGTGCCAATT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   912 ATACAAAAAGTGAGATTCAGGGAAGTGCCACCAAGATCAAGGATATCTGTGCCAATT 971

Qy   961 AAAAGGAATGCTATATTGCATAGAAATGAATGGGAGACCACCAGCTGGAGCCCAGAAGGCC 1020
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Db   972 AAAAGGAATGCTATATTGCATAGAAATGAATGGGAGACCACCAGCTGGAGCCCAGAAGGCC 1031

Qy  1021 AGATCATAAAAATGATAGAAAGACCCAAAATTGCTGCTGTCGTGGACATTATGATTAT 1080
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Db  1032 AGATTTATAAAAATGATAGAAAGAAGACCCAAAATTGCTGCTGTCGTGGACATTATGATTAT 1091

Qy  1081 TATTATGCTCAACTTGATATGCTGATGCTGGGAGGAGACGCCCACAAGTTATCACCCTATT 1140
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Db  1092 TATTATGCTCAACTTGATATGCTGATGCTGGGAGGAGACGCCCACAAGTTATCACCCTATT 1151

Qy  1141 CCTCAGAGAAATACTGGAGTTGAGGATTACGGTCAGGAAGCATGGTCATCGTCCATCCCCA 1200
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Qy  1201 AGTCAATGGCCTGCTCGAGTTACCTTCAGAGAAAATTTGAAGCTCAACAATATAAGTTGAAA 1260
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Db  1212 AGTCAATGGCCTGCTCGAGTTACCTTCAGAGAAAATTTGAAGCTCAACAATATAAGTTGAAA 1271

Qy  1261 GTGGAGAAGCAATTGGGTCTTCGTCCCATCTTCGTCCATCTCTGTCGAGCCAAATTACACCAGAGACAA 1320
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Qy  1321 GAGCTAAGAGTAATGGAGAATATTGGAAGCAGTTAGAGGAAAATACGCCACCAGTTACCAATGAC 1380
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Qy  1381 ATGAAGGAACAGGAATATTGGAAGCAGAATGGGGAGAAGATGGGGAGAGAACTCAAAAATAAGTCAT 1440
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Qy  1441 ATGAAAGAAATTAGAAGAAGATGGGGAGAAAGAAGATGGGGAGAGAACCAG----------------- 1488
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Db  1452 ATGAAAGAAATTAGAAGAAGATGGGGAGAAAGAAGATGGGGAGAGAACCAG 1488

Qy  1501 AAAACCTATTGGTGAAGAAGAGTAACCTGCCTGTCCATCAAGAGTGCATCTGAGGGAGAA 1560
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Db  1489 ---------------------------------------------------- 1488

Qy  1561 GCACCTGTCGCAGGACATTGAAAGACTTGAAACAAATGAGGGCTTCAGAAACACAAAAGGAA 1620
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Db  1489 ------AGGACATTGAAAGACTTGAAACAAATGAGGGCTTCAGAACAACACAAAGGAA 1538

Qy  1621 AGTAAAAATCCAGAACAGAATATAAAGCTAAGAGGGGTAAAATTGAAATTAATTTA 1680
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Qy  1681 GACAAATGTATTTCTGATGAAGCATGAAGCTTAAGGAAGTTAAGGAATGTGTAAAGGAGCAT 1740
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Db  1599 GACAAATGTATTTCTGATGAAGCATGAAGCTTAAGGAAGTTAAGGAATGTGTAAAGGAGCAT 1658

Qy  1741 GAAACTTTGACCTTTGAGGATGGCATGAAGTGAAGTTTAAGGAATGAATGTGTAAAGGAGCAT 1800
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Db  1659 GAAACTTTGACCTTTGAGGATGGCATGAAGTGAAGTTTAAGGAATGAATGTGTAAAGGAGCAT 1718
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Qy  1801 GGAGATTATACAGACAAAGCATTTGAAAAACTTCACTGCCCAGAAGCAGGTTTTCCACG 1860
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Db  1719 GGAGATTATACAGACAAAGCATTTGAAAAACTTCACTGCCCAGAAGCAGCAGCATTTACAGAA 1778

Qy  1861 CAGACT 1866
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Db  1779 CTGACT 1784
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RESULT 7
AX166554
LOCUS   AX166554   1947 bp   DNA   linear   PAT 22-JUN-2001
DEFINITION Sequence 45 from Patent WO0138503.
ACCESSION   AX166554
VERSION   AX166554.1 GI:14546899
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
            Flanagan,P. and Clary,D.S.
  TITLE   Novel human protein kinases and protein kinase-like enzymes
  JOURNAL   Patent: WO 0138503-A 45 31-MAY-2001;
            Sugen, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..1947
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   71.6%; Score 1469.6; DB 6; Length 1947;
Best Local Similarity   87.0%; Pred. No. 0;
Matches 1721; Conservative   0; Mismatches   89; Indels 168; Gaps   3;

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Qy    1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGACGTGCCTTCGGGAAAGCATACTTA   60
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Db    1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGACGTGCCTTCGGGAAAGCATACTTA   60

Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG  120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG  120

Qy  121 CCCATACAAGAGAAAAGAAGCTTCAAAGAAGAAGATCATGAAAAGATGAGTAGAGTAAGATGAAACAT  180
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Db  121 CCCATACAAGAGAAAAGAAGCTTCAAAGAAGAAGATCATGAAAAGATGAGTAGAGTAAGATGAAACAT  180

Qy  181 CCCACACATTGTAGCCTTCTCAATTCATTTCAGAGAATGGCAGGCTGTTATTGTAATG  240
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Db  181 CCCACACATTGTAGCCTTCTCAATTCATTTCAGAGAATGGCAGGCTGTTATTGTAATG  240

Qy  241 GAATATTGTGATGAGGGGGATCTCATGAAAAGGATCAATAGACAACGGGTGTGTTATTT  300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GAATATTGTGATGAGGGGGATCTCATGAAAAGGATCAATAGACAACGGGTGTGTTATTT  300

Qy  301 AGTGAAGATCAGATCCTCGTTGGTTTGTACAGGGACATAAAAGCTTCTTAGCAACATATTCAT  360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AGTGAAGATCAGATCCTCGTTGGTTTGTACAGGGACATAAAAGCTTCTTAGCAACATATTCAT  360

Qy  361 GACAGGAAGAGATATTACACAGGGACACTTGGGACTTTGGTATAGCAAGAGTCCAGAACATTTCTTAGCAACGAACGGA  420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GACAGGAAGAGATATTACACAGGGACACTTGGGACTTTGGTATAGCAAGAGTCCAGAACATTTCTTAGCAACGAACGGA  420

Qy  421 ATGGTGGCAAAGCTTGGGGACTTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480
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Db  421 ATGGTGGCAAAGCTTGGGGACTTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480

Qy  481 GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCCTGAGAATAAACCC  540
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Db  481 GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCCTGAGAATAAACCC  540
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Qy  541 TACAACAATAAAACGGTATATTGGTCTCTTGGCTGTGTCTTATATGAGCTCGCACACTT  600
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Db  541 TACAACAATAAAACGGTATATTGGTCTCTTGGCTGTGTCTTATATGAGCTCGCACACTT  600

Qy  601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAAGCACAT  660
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Db  601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAAGCACAT  660

Qy  661 TTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTCGATATCTCAGCTCTT  720
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Db  661 TTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTCGATATCTCAGCTCTT  720

Qy  721 CAAGTATCCTCCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTAGAG  780
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Db  721 CAAGTATCCTCCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTAGAG  780

Qy  781 AATCTTATTCCCAAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT  840
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Db  781 AATCTTATTCCCAAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT  821

Qy  841 ATATGCAGAGCAGGAGCGCCAGCTTCTGACATGCTGGGAAGGTGGTCAGAAGTGTAA  900
        |  |||    ||
Db  822 ------------GGTGACTGTTGGATTTTGGCAGAGATTTGGGTTGCAGGTCCTTG  867

Qy  901 ATACAAAAGTGAGATTCCAGGGAAAGTGCCCACCAGAGATCAAGGATATCTGTGCCAATT  960
        |||||||||||||||||||||||||||||||||||||||||||
Db  868 ACAGTGTGTTCGGTTTAGGTGTGAGCCACTGCACCCAGCCTGTATTATGGTTTTTAA  927

Qy  961 AAAAGGAATGCTATATTGCCATGAAAATGAATGAGAACCACCAGCTGGAGCCTGGAGCCCAGAAGGCC 1020
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Db  928 AACATCCCCTCTTGTTTTCTT  948

Qy 1021 AGATCTATAAAAATGATAGAAAGACCCAAAATTGCTGCTGTCTGTGGACATTATGATTAT 1080
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  949 ---CAGATAAAAATGATAGAAAGACCCAAAATTGCTGCTGTCTGTGGACATTATGATTAT 1005

Qy 1081 TATTTATGTCAACTTGATATGTCGAGGAGAGCCCACAACCAAGTTATCACCCTATT 1140
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Db 1006 TATTTATGTCAACTTGATATGTCGAGGAGAGCCCACAACCAAGTTATCACCCTATT 1065

Qy 1141 CCTCAAGAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCGTCCATCCCCA 1200
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1066 CCTCAAGAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCGTCCATCCCCA 1125

Qy 1201 AGTCAAGAGCCTGCTGAGTACCTTCAGAGAAAATTTGAAGCTCAACAATATAAGTTGAAA 1260
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Db 1126 AGTCAAGAGCCTGCTGAGTACCTTCAGAGAAAATTTGAAGCTCAACAATATAAGTTGAAA 1185

Qy 1261 GTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA 1320
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1186 GTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA 1245

Qy 1321 GAGCTAAGAAGTAATGAGAAGAGCCTAGAATTCCAGGAGCTGCCATTAGGAAAAACGAA 1380
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Db 1246 GAGCTAAGAAGTAATGAGAAGAGCCTAGAATTCCAGGAGCTGCCATTAGGAAAAACGAA 1305

Qy 1381 ATGAAGGAACAGGAATATTGGAAGCAGTTAGAGGAAATACGGCCAAGTACCACCAATGAC 1440
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Db 1306 ATGAAGGAACAGGAATATTGGAAGCAGTTAGAGGAAATACGGCCAAGTACCACCAATGAC 1365

Qy 1441 ATGAAAAGAAATTAGAAAGAAATTAGAAAGAAATGGGGAGAAGAACCCAGAGGAGACCGGA 1500
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Db 1366 ATGAAAAGAAATTAGAAAGAAATTAGAAAGAAATGGGGAGAAGAACCGA  1402

Qy 1501 AAAACCTATTTGGTGAAGAAGAGTAACCTGCCTGTCCATCAAGATGCATCTGAGGGAGAA 1560
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Db 1403 ----------------------------------------------  1402

Qy 1561 GCACCTGTGCAGGACATTGAAACAAATGAAGCTTCAGAACAACAAAAGGAA 1620
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Db 1403 --------------AGGACATTGAAACAACTTCAGAACAACAAAAGGAA  1452

Qy 1621 AGTAAAAATCCAGAACAGAAACAGAAATATAAAGCTAAGAAGGGGTAAAATTGAAATTAATTTA 1680
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Db   301  AGTGAAGATCAGATCCTCGGTTGGTTGTTGTACAGATTTCTCTAGAGACTAAAACATATTCAT  360
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Qy   361  GACAGGAGAGATATTACACAGGGACATAGGGGTAAGCTAGGAAGAGAGGCAATGCAAGAACGGA  420
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Db   361  GACAGGAGAAGATATTACACAGGGACATAGGGGTAAGCTAGGAAGAGAGGCAATGCAAGAACGGA  420

Qy   421  ATGGTTGGCAAAGCTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480
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Db   421  ATGGTTGGCAAAGCTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480

Qy   481  GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCGTCAGAATAAAACCC  540
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Db   481  GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCGTCAGAATAAAACCC  540

Qy   541  TACAACAATAAAACCGATATTGGTCTCTTGGCTGTCTTATATGAGTCTGCACACTT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TACAACAATAAAACCGATATTGGTCTCTTGGCTGTCTTATATGAGTCTGCACACTT  600

Qy   601  AAACATCCTTTGAGGGTAACAACTTACAGCAGTTGGTTCTGAAGATTTGTCAAGCACAT  660
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Db   601  AAACATCCTTTGAGGGTAACAACTTACAGCAGTTGGTTCTGAAGATTTGTCAAGCACAT  660

Db   661  TTTGCCCAATATCTCCGGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCCAGCTCTTT  720
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Qy   721  CAAGTATCTCCTCGAGACCGACATCCATCCATTTGAAAAGGCCCTTTTTAGAG  780
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Qy   781  AATCTTATTCCACATCCCAAATATTTGACTCCTGAGTCATTCAGGAAGAATTCAGTCACATGCTT  840
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Db   781  AATCTTATTCCACATCCCAAATATTTGACTCCTGAGTCATTCAGGAAGAATTCAGTCACATGCTT  840

Qy   841  ATATGCAGAGCGAGAGCGAGGCCAGCTTCTGACATGTGGGAAGGTGGTCCAGAAGTGTA-A  899
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  ATATGCAGAGCGAGAGCGAGGCCAGCTTCTGACATGTGGGAAGGTGGTCCAGAGGCATACT  900

Qy   900  AATACAAAAGTGAGATTCCAGGGAAAGTGCCACCAAGATCAAGGATATCTGTGCCAAT  959
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Db   901  GGTGTGAGGAGTGGGCTCTCAAGGGCTTGGCAGTCTGCTCGTCCTGAGGCTTGCAGGCTA  960

Qy   960  TAAAAGGAATGCTATATTGCATAGAAATGAATGAGACCCAGCTGGAGCCCAGAAGGC  1019
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Db   961  CAGCCCCTGCGGCGTCTCTCACAGG--------CTGCTGTTGAGTGTCTGCGGCT  1007

Qy   1020 CAGATCTATAAAAATGATAGAAAGACCCAAAATTGCTGCTGTCTGTGACATTATGATTA  1079
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Db   1008 TTTCCAGATAAAAATGATAGAAAAGAGCCCAAAATTGCTGCTGTCTGTGACATTATGATTA  1067

Qy   1080 TTATTATGCTCAACTTGATATGCTGAGAGGAGCCCCACAAACCAAGTTATCACCCTAT  1139
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1068 TTATTATGCTCAACTTGATATGCTGAGAGGAGCCCCACAAACCAAGTTATCACCCTAT  1127

Qy   1140 TCCTCAAGAAATACTGGAGTTGAGGATTACGGTCAAGAGGCATGGTCCATCCCC  1199
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1128 TCCTCAAGAAATACTGGAGTTGAGGATTACGGTCAAGAGGCATGGTCCATCCCC  1187

Qy   1200 AAGTCAATGGCCTGCTGAGTACTTCAGAGAAATTTGAAGCTCAACATATAAGTTGAA  1259
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Db   1188 AAGTCAATGGCCTGCTGAGTACCTTCAGAGAAAAATTTGAAGCTCAACATATAAGTTGAA  1247

Qy   1260 AGTGGAGAGCAATGGGTCTTCGTCCTCATCTTCTGCCGAGCCAAATTACAACCAGAGACA  1319
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Db   1248 AGTGGAGAGCAATT----------------------------------------------  1262

Qy   1320 AGAGCTAAGAGTAATGGAGAGAATGGCAGGCTAGATTCCAGGAGCTGCCATTAGGAAAAACGA  1379
          
Db   1263 ------------------------------------------------------------  1262

Qy   1380 AATGAAGGAACAGGAATATTGGAAGCAGTTAGAGAGGAAATACGCCAACAGTACCACCAATGA  1439
          
Db   1263 -----GGAATATTGGAAGCAGTTAGAGAGGAAATACGCCAACAGTACCACCAATGA  1310
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RESULT 8
AX659636
LOCUS       AX659636                    1896 bp    DNA        linear       PAT 22-MAR-2003
DEFINITION  Sequence 1 from Patent WO03000903.
ACCESSION   AX659636
VERSION     AX659636.1  GI:29161818
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human nek-like serine/threonine protein kinase
  JOURNAL   Patent: WO 03000903-A 1 03-JAN-2003;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match       66.3%;    Score 1359.8;  DB 6;  Length 1896;
Best Local Similarity  84.5%;  Pred. No. 2.6e-309;
Matches 1673;    Mismatches  302;    Conservative  0;    Indels  224;    Gaps  4;
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Qy     1  ATGGGATAAGTACGATGTGATTAAGGCACCATCCGGCAAGGTGCCTTCGGCGAAAGCCATACTTA  60
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Db     1  ATGGGATAAGTACGATGTGATTAAGGCACCATCCGGCAAGGTGCCTTCGGCGAAAGCCATACTTA  60

Qy    61  GCTAAAGGGAAATCAGATAGCAAGCACTCTGTCTCATGAAAGAGATCAATTTGAAAAGATG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GCTAAAGGGAAATCAGATAGCAAGCACTCTGTCTCATGAAAGAGATCAATTTGAAAAGATG  120

Qy   121  CCCATACAAGAAAAGAAGCTTCAAAGAAAGAAGAGTCTTCTTCTGAAAAGATGAAACAT  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CCCATACAAGAAAAGAAGCTTCAAAGAAAGAAGAGTGATTCTTCTGAAAAGATGAAACAT  180

Qy   181  CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAAGAATGGCAGGCGTGTTTATTGTAATG  240
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Db   181  CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAAGAATGGCAGGCGTGTTTATTGTAATG  240

Qy   241  GAATATTGTGATGGAGGGGATCCATGAAAGAAGGATCAATAGACAACGGGGTGTGTTATTT  300
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Db   241  GAATATTGTGATGGAGGGGATCCATGAAAGAAGGATCAATAGACAACGGGGTGTGTTATTT  300

Qy   301  AGTGAAGATCAGATCCTCGGTTGGTTGTTGTACAGATTCTCTAGAGACTAAAACATATTCAT  360
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Db   1453 -----------------------------------------------------------  1512
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Qy   1681 GACAAATGTATTTCTGATGAAAACATCCTCCAAGATGAAGAGGCAATGCAATGGTATACCAAAT  1740
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Db   1513 GACAAATGTATTTCTGATGAAAACATCCTCCAAGATGAAGAGGCAATGCAATGGTATACCAAAT  1572

Qy   1741 GAAACTTTGACCTTGAGGATGCATGAAGTTTAAGGAATATGAAATGTGTAAAGGAGCAT  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1573 GAAACTTTGACCTTGAGGATGCATGAAGTTTAAGGAATATGAAATGTGTAAAGGAGCAT  1632

Qy   1801 GGGAGATTATACAGACAAAGCATTTGAAAAACTTCACTGCCCAGAAGCAGGGTTTTCCACG  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1633 GGGAGATTATACAGACAAAGCATTTGAAAAACTTCACTGCCCAGAAGCAGGGTTTTCCACG  1692

Qy   1861 CAGACTGTAGCTGCTGTGTGGGAAACAGGAGGCAGTGGGATGGGAGAGGAGGAGCGCCTCAGACTCTG  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1693 CAGACTGTAGCTGCTGTGTGGGAAACAGGAGGCAGTGGGATGGGAGAGGAGGAGCGCCTCAGACTCTG  1752

Qy   1921 CTTGCAGATGATGGCAGTGGCCGACATCACCTCCCACCTGCCCCGCACGGGGCCTGACAGTG  1978
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1753 CTTGCAGATGATGGCAGTGGCCCGACATCACCTCCCACCTGCCCCGCACGGGGCCTGACAATG  1810
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RESULT 9
AX659639

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LOCUS       AX659639                1918 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 4 from Patent WO03000903.
ACCESSION   AX659639
VERSION     AX659639.1  GI:29161819
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human nek-like serine/threonine protein kinase
  JOURNAL   Patent: WO 03000903-A 4 03-JAN-2003;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1..1918
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             66.3%;  Score 1359.8;  DB 6;  Length 1918;
Best Local Similarity   84.5%;
Matches 1673;  Conservative   0;  Mismatches  82;  Indels 224;  Gaps  4;  Pred. No. 2.6e-309;
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                                    /mol_type="unassigned DNA"
                                    /db_xref="taxon:9606"

ORIGIN

              Query Match        38.8%;   Score 797.2; DB 6;  Length 1884;
              Best Local Similarity  74.7%;  Pred. No. 8.1e-177;
              Matches 1249;  Conservative  0;  Mismatches  3;  Indels 420;  Gaps  3;

Qy    307 GATCAGATCCTCCGGTTGGTTGTACAGATTCTCCAGGACTAAAACATATTCATGACAGAG 366
          ||||||||||||||||| |||||||||| |||||||||||||||| |||||||||||||
Db    112 GAAAAGATCCTCCGGTTGGTTGTACAGATTTCTCCAGGACTAAAACATATTCATGACAGAG 171

Qy    367 AAGATATTACACAGGGACATTAGAGGAAATACCGCCAACAGTACCACAATGA 426
          |||||||||||||||||||||| |||||| ||||||||||||||||||||||
Db    172 AAGATATTACACAGGGACATTAGAGGAAATACCGCCAACAGTACCACAATGA 231

Qy    427 GCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAATTCATGGAGACTTGCTCGA 486
          |||||||||||||||||||||||||||||||
Db    232 GCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAA----------------- 272

Qy    487 ACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCCTACAAC 546
Db    273 ----------------------------------------------------------- 272

Qy    547 AATAAAACGATATTTGGTCTTTGGCTGTCTTATATGAGCTCTGACACTTAAACAT 606
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    273 ------GGATATTTGGTCTTTGGCTGTCTTATATGAGCTCTGACACTTAAACAT 324

Qy    607 CCTTTTGAGGTAACAACTTACAGCAGCTGGTTCTGGAGCTCCATTCGTTCAAGCACATTTTGCC 666
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    325 CCTTTTGAGGTAACAACTTACAGCAGCTGGTTCTGGAGCTCCATTCGTTCAAGCCACATTTTTGCC 384

Qy    667 CCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTTCAAGTA 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 CCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTTCAAGTA 444

Qy    727 TGAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGAATGTGTAAAGGAGCA 786
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 TCTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTTATATGC 504

Qy    787 ATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTTATATGC 846
          ||||||||||||||||||
Db    505 ATTCCCAAATATTTGACTCCTGAG---------------------------------- 528

Qy    847 AGAGCAGGAGCGCCAGCTTCTGCACATGCTGGGAAGGTGGTCCAGAAGTGTAAAATACAA 906
Db    529 ----------------------------------------------------------- 528

Qy    907 AAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATCAAGGATATCTGTGCCAATTAAAAGG 966
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 ----------------------------------------------------------- 528

Qy    967 AATGCTATATTGCATAGAAATGACTAGAGAATGAATGAGAGGCCCAGAAGGCCAGATCT 1026
Db    529 ----------------------------------------------------------- 528

Qy   1027 ATAAAAATGATAGAAAGACCCAAAATTGCTGCTGTCTGGACATTATGATTATTATTATTAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 ATAAAAATGATAGAAAGACCCAAAATTGCTGCTGTCTGTGACACATTATGATTATTATTATTAT 588

Qy   1087 GCTCAACTTGCTGATATGCTGAGGAGGAGAGCCCACAAACCAAGTTATCACCCTATTCCTCAA 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    589 GCTCAACTTGATATGCTGAGGAGGAGAGCCCACAAACCAAGTTATCACCCTATTCCTCAA 648

Qy   1147 GAAAATACTCGAGTTGAGATTACCGTCAGGAAACGAGGCATGGTCCATCCCCAAGTCAA 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    649 GAAAATACTCGAGTTGAGATTACCGTCAGGAAACGAGGCATGGTCCATCCCCAAGTCAA 708

Qy   1207 TGGCCTGCTGAGTACTTCAGGAAAAATTTGAAGCTCAACAATAAGTTGAAAGTGGAG 1266
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    709 TGGCCTGCTGAGTACTTCAGGAAAAATTTGAAGCTCAACAATAAGTTGAAAGTGGAG 768

Qy   1267 AAGCAATTGGGTCTTCGTCGTCCATCTTCTGCCGAGCCAAATTACACCAGAGACAAGAGCTA 1326
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Db   1210 AAGTCAATGGCCTGCTGAGTACCTTGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACA 1269
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   1260 AGTGGAGAAGCAATGGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACA 1319
          ||||||||||||||||
Db   1270 AGTGGAGAAGCAATT------------------------------------------------ 1284

Qy   1320 AGAGCTAAGAAGTAATGGAGAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAAAAACGA 1379
Db   1285 ----------------------------------------------------------- 1284

Qy   1380 AATGAAGGAACAGGAATATTGGAGGCAGTTAGAGGAAATACCGCCAACAGTACCACAATGA 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1285 ------GGAATATTGGAAGCAGTTAGAGGAAATACCGCCAACAGTACCACAATGA 1332

Qy   1440 CATGAAAGAAATTAGAAGAAGATGGGGAGAGAACCAGAGGAGAACTCAAAAATAAGTCA 1499
          ||||||||||||||||||||||||||
Db   1333 CATGAAAGAAATTAGAAGAAGATGGGGAGAGAACCAG---------------------- 1370

Qy   1500 TAAAACCTATTTGGTGAAGAAGTAACCTGCCTGTCCATCAAGATGCATCTGAGGGAGA 1559
Db   1371 ----------------------------------------------------------- 1370

Qy   1560 AGCACCTGTGCAGGACATTGAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGA 1619
          ||||||||||||||||||||||||||||||||||||||||||
Db   1371 ------AGGACATTGAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGA 1419

Qy   1620 AGTAAAAATCCAGAACAGAATATAAAGCTAAGAGGGGGTAAATTTGAAATTAATTT 1679
          ||||||||||||||||||||||||||||||||||||||||||
Db   1420 AGTAAAAATCCAGAACAGAATATAAAGCTAAGAGGGGTAAAATTTGAAATTAATTT 1479

Qy   1680 AGACAAAATGTATTTCTGATGAAAACATCCTCCAAGAGGAAGAGGCAATGGATATACCAAA 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 AGACAAAATGTATTTCTGATGAAAACATCCTCCAAGAGGAAGAGGCAATGGATATACCAAA 1539

Qy   1740 TGAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGAATGTGTAAAGGAGCA 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TGAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGAATGTGTAAAGGAGCA 1599

Qy   1800 TGGAGATTATACAGACAAAGCATTGAAAAATTCACTGCCCAGAAGCAGGGTTTTCCAC 1859
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 TGGAGATTATACAGACAAAGCATTGAAAAATTCACTGCCCAGAAGCAGGGTTTTCCAC 1659

Qy   1860 GCAGACTGTAGCTGCTGTGGGAAACAGAGGCAGTGGGATGGAGGAGCGCCTTCAGACTCT 1919
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 GCAGACTGTAGCTGCTGTGGGAAACAGAGGCAGTGGGATGGAGGAGCGCCTTCAGACTCT 1719

Qy   1920 GCTGCAGATGATGGCAGTGGCCGACATCCACCTCCACCTGCCCCACCTGCCCCTGACAGTG 1978
          ||||||||||||||||||||||||||||||||||||||| ||
Db   1720 GCTGCAGATGATGGCAGTGGCCGACATCCACCTCCACCTGCCCCACCTGCCCCTGACAATG 1778
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RESULT 10
LOCUS   CQ732078   1884 bp   DNA   linear   PAT 03-FEB-2004
DEFINITION Sequence 18012 from Patent WO02068579.
ACCESSION   CQ732078
VERSION   CQ732078.1   GI:42310392
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE   Kits, such as nucleic acid arrays, comprising a majority of
            human exons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 18012 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES   Location/Qualifiers
     source   1..1884
                     /organism="Homo sapiens"

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Best Local Similarity  99.6%;  Pred. No. 7.4e-175;
Matches  801;  Conservative  0;  Mismatches  2;  Indels  2;  Gaps  1;

Qy   771  CTTTTTAGAGAATCTTATTCCCAAATATTTGACTTCCTGAGCTCATTCAGGAGGAGAATTCAG  830
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||  ||||||||
Db     1  CTTTTTAGAGAATCTTATTCCCAAATATTTGACTTCCTGAGGTCATTCAGGAAGAATTCAG   60

Qy   831  TCACATGCTTATATGCAGGAGGAGGCCAGCTTCTCGACAGTCGTGGGAAGGTGGTCCA     890
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    61  TCACATGCTTATATGCAGGAGGAGGGCCAGCTTCTCGACAGTCGTGTGGGAAGGTGGTCCA  120

Qy   891  GAAGTGTAAAATCAAAAAGTGAGATTCCAGGGAAGTGCCCACCAAGTCAAGGAGATATC     950
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GAAGTGTAAAATCAAAAAGTGAGATTCCAGGGAAGTGCCCACCAAGTCAAGGAGATATC   180

Qy   951  TGTGCCAATTAAAAGGAATGCTATATTGCATGAAATGAAATGAATGAGACCACCAGCTGGAGC  1010
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TGTGCCAATTAAAAGGAATGCTATATTGCATGAAATGAAATGAATGAGACCACCAGCTGGAGC   240

Qy  1011  CCAGAAGGCCAGATCTATAAAAAGTCAGAACACAAAGGAAAGTAAACTGTCTGTGTCTGTGGACA  1070
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CCAGAAGGCCAGATCTATAAAAAGTCAGAACACAAAGGAAAGTAAACTGTCTGTGTCTGTGGACA   300

Qy  1071  TTATGATTATTATTATGCTCAACTTGATATGTCGAGAAATTTGAAATTAATTTAGACAAA  1130
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  TTATGATTATTATTATGCTCAACTTGATATGTCGAGAAATTTGAAATTAATTTAGACAAA   360

Qy  1131  TCACCCTATTCCTCAAGAAAATACTGGAGTTGAGGATTACGGTTCAGGAAAACGAGGGCATGG  1190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  TCACCCTATTCCTCAAGAAAATACTGGAGTTGAGGATTACGGTTCAGGAAAACGAGGGCATGG   420

Qy  1191  TCCATCCCAAGTCAATGGCCTGCTGCTGCGAGAAATTTGAAGCTCAACAATA  1250
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  TCCATCCCAAGTCAATGGCCTGCTGCTGCGAGAAATTTGAAGCTCAACAATA   480

Qy  1251  TAAGTTGAAAGTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAA  1310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TAAGTTGAAAGTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAA   540

Qy  1311  CCAGAGCAAGAGCTAAGAAGTAATGAAGCAGGAATATTGGAAGCAGTGAGGAAATACGCCAAGTA  1370
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  CC-GAGCAAGAGCTAAGAAGTAATGAAGCAGGAATATTGGAAGCAGTGAGGAAATACGCCAAGTA   599

Qy  1371  GAAAAACGAAATGAAGGAACAGGAATTAGAAAGAAATTAGAAAGAAAGATGGGGAGAAGAACTCAAA  1430
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   600  GAAAAACGAAATGAAGGAACAGGAATTAGAAAGAAATTAGAAAGAAAGATGGGGAGAAGAACTCAAA   659

Qy  1431  CCACAATGACATGAAAGAAATTAGAAAGAAATTAGAAAGAAAGAAGAGAGGGAGAGAACCAGAGGAGAACTCAAA  1490
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   660  CCACAATGACATGAAAGAAATTAGAAAGAAATTAGAAAGAAAGAAGAGAGGGAGAGAACCAGAGGAGAACTCAAA   719

Qy  1491  AATAAGTCATAAAACCTATTTGGTGAAGAAGTAACCTGCCTGTCCATCAAGATGCATC  1550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   720  AATAAGTCATAAAACCTATTTGGTGAAGAAGTAACCTGCCTGTCCATCAAGATGCATC   779

Qy  1551  TGAGGGAAGCACCTGTGCAGGA   1574
          |||||||||||||||||||||
Db   780  TGAGGGAGGCACCTGTGCAGAA   803
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RESULT 12

AK126330

LOCUS   AK126330   3635 bp   mRNA   linear   PRI 09-SEP-2003

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Db   769  AGCAATT-------                                                 776
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Qy  1327  AGAAGTAATGGAGAAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAAAAACGAAATGAAG  1386

Db   777  ------------------------------------------                    776

Qy  1387  GAACAGGAATAATTGGAAGCAGTAGAGGAAATACGCCAACAGTCGACACCAGTGACTACACGAA  1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   777  ----GGAATAATTGGAAGCAGTAGAGGAAATACGCCAACAGTCGACACCAGTGACTACACGAA   831

Qy  1447  GAAATTAGAAAGAAGATGGGGAGAACCAGAGGAGAACTCAAAAATAAGTCATAAAAACC  1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   832  GAAATTAGAAAGAAGATGGGGAGAACCAGAGGAGAACTCAAAAATAAGTCATAAAAACC   891

Qy  1507  TATTTGGTGAAGAAGTAACCTGCCTGTCCATCAAGATGCATCTGAGGGAGAAGCACCT  1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   892  TATTTGGTGAAGAAGTAACCTGCCTGTCCATCAAGATGCATCTGAGGGAGAAGCACCT   951

Qy  1567  GTGCAGGACATTGAAAAAGACTTGAAACAAATGAAACAAATGAAGGAAAGTAAA  1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   952  GTGCAGGACATTGAAAAAGACTTGAAACAAATGAAACAAATGAAGGAAAGTAAA  1011

Qy  1627  AATCCAGAACAGAAATATAAAGCTAAGAAGGGGTAAAATTTGAAATTAATTTAGACAAA  1686
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1012  AATCCAGAACAGAAATATAAAGCTAAGAAGGGGTAAAATTTGAAATTAATTTAGACAAA  1071

Qy  1687  TGTATTTCTGATGAAAAGATCTCCTCCAAGAGGAGGCAATGGCATGAGGCATGAAACT  1746
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1072  TGTATTTCTGATGAAAAGATCTCCTCCAAGAGGAGGCAATGGCATGAGGCATGAAACT  1131

Qy  1747  TTGACCTTTGAGGATGGCATGAGAAGTTAAGGAAGTTGTAAAGGAGCATGTGAGAT  1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1132  TTGACCTTTGAGGATGGCATGAGAAGTTAAGGAAGTTGTAAAGGAGCATGTGAGAT  1191

Qy  1807  TATACAGACAAAAGCATTTGAAAAACTTCACTGCCCAGAAGCCAGGGTTTTCCACGCGACT  1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1192  TATACAGACAAAAGCATTTGAAAAACTTCACTGCCCAGAAGCCAGGGTTTTCCACGCGACT  1251

Qy  1867  GTAGCTGCTGTGGGAAAACAGGAGGCCAGTGGACATGGGAGGCGCCTCCACCTGCTCGCAG  1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1252  GTAGCTGCTGTGGGAAAACAGGAGGCCAGTGGACATGGGAGGCGCCTCCACCTGCTCGCAG  1311

Qy  1927  ATGATGGCAGTGGCCGACATCACCTCCACCTGCCCCACGGGGGCCTGACAGTG  1978
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db  1312  ATGATGGCAGTGGCCGACATCACCTCCACCTGCCCCACGGGGGCCTGACAATG  1363
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RESULT 11

CQ843384

LOCUS   CQ843384   3635 bp   DNA   linear   PAT 02-AUG-2004

FEATURES   Location/Qualifiers
     source   1..3635
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match 38.4%; Score 788.8; DB 6; Length 3635;

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Qy   1131 TCACCCTATTCCTCAGAAAATACTGGAGTTGAGATTACGGTCAGGAAACGAGGCATG 1190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TCACCCTATTCCTCAGAAAATACTGGAGTTGAGATTACGGTCAGGAAACGAGGCATG  420

Qy   1191 TCCATCCCAAGTCAATGGCCTGCTGAGTACCTTCAGAGAAAATTTGAGCTCAACAATA 1250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCCATCCCAAGTCAATGGCCTGCTGAGTACCTTCAGAGAAAATTTGAGCTCAACAATA  480

Qy   1251 TAAGTTGAAAGTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAA 1310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TAAGTTGAAAGTGGAGAAGCAATTGGGTCTTTCGTCCATCTTCTGCCGAGCCAAATTACAA  540

Qy   1311 CCAGAGACAAGAGCTAAGAGTAATGGAGAGAGAGCTAGATTCCAGGAGCTGCCATTTAG 1370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CC-GAGCACAGAGCTAAGAGTAATGGAGAGAGAGCTAGATTCCAGGAGCTGCCATTTAG  599

Qy   1371 GAAAAACGAAATGAAGGAACAGAGGAATATTGGAAGCAGTAGAGGAAATACGCCAACAGTA 1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 GAAAAACGAAATGAAGGAACAGAGGAATATTGGAAGCAGTAGAGGAAATACGCCAACAGTA  659

Qy   1431 CCACAATGACATGAAGAAATTAGAAAGAAGATGGGAGGAGAACCAGAGGAGAACTCAAA 1490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 CCACAATGACATGAAGAAATTAGAAAGAAGATGGGAGGAGAACCAGAGGAGAACTCAAA  719

Qy   1491 AATAAGTCATAAAACCTATTTGGTGAAGAGAGTAACCTGCCTGTCCATCAAGATGCATC 1550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 AATAAGTCATAAAACCTATTTGGTGAAGAGAGTAACCTGCCTGTCCATCAAGATGCATC  779

Qy   1551 TGAGGGAGAAGCACCTGTGCAGGA 1574
          ||||||||||||||||||||||||
Db    780 TGAGGGAGAAGCACCTGTGCAGAA  803
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RESULT 13
AX803389

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LOCUS       AX803389               1632 bp    DNA            linear    PAT 24-NOV-2003
DEFINITION  Sequence 51 from Patent WO3000901.
ACCESSION   AX803389
VERSION     AX803389.1  GI:38502052
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Martinez,R.A. and Sigurdsson,G.T.
  TITLE     Nucleic acids encoding protein kinases
  JOURNAL   Patent: WO 0300901-A 51 03-JAN-2003;
            Decode Genetics EHF. (IS)
FEATURES             Location/Qualifiers
     source          1..1632
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             <1..>1632
                     /note="MOOSE03455"
                     /codon_start=1
                     /product="OPK V NimA family"
                     /protein_id="CAE55983.1"
                     /db_xref="GI:38502053"
                     /translation="YRNVSRAHERLHSCLVGLGVFLRGVAYRAKRERDGEWLLSGAVK
                     KHMALIKNMADKYLKSFQHQMIPFLTENGRLFIVMEYCDGGDLMKRINRQGVLFSED
                     QILGWFVQISLGLKHIHDRKILHRDIKAQNIFLSKNGMVAKLGDFGIARVLNNSMELA
                     RTCIGTPYYLSPEICQNKPYNNKTDIWSLGCVLYELCTLKHPFEGNNLQLVLKICQA
                     HFAPISPGFSRELHSLISQLFQVSPRDRPSINSILKRPFLENLIPKYLTPEVSFEYLQ
                     RKFEAQQYKLKVEKQLVSKGYLRQNLSAVELILKNLLKAPHWKFIIPSPKKVSRVGT
                     DHCFFRRASHEIASLYAQFHMAGEASQSWQKAKEEQSHALHEGRQESLWELLFTKPSD
                     LLKAAVSHDCATVPQPGIQSKTRSQKNKALITSQTGRRGKGAPHISDDGRPGRDAPHF
                     LDGMAAGQRRSSLSRLGSQAEGLLTSQTGMGGRAETLLTSQTGRLRQENCLNLGGGGCSE
                     PRSSGERGHPCLVPVFKGNASSFCPFKNKDSVRVVR"
ORIGIN
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Query Match             38.4%;  Score 788.8;  DB 9;  Length 3635;
Best Local Similarity   99.6%;  Pred. No. 7.4e-175;
Matches  801;  Conservative   0;  Mismatches   2;  Indels  1;  Gaps   1;

Qy    771 CTTTTAGAAGAATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGAATTCAG  830
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTTTTTAGAAGAATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGAATTCAG   60

Qy    831 TCACATGCTTATATGCGAGAGCAGGAGGCGCCAGCTTCTCGGACATGCTGGGAGGTGGTCCA  890
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCACATGCTTATATGCGAGAGCAGGAGGCGCCAGCTTCTCGGACATGCTGGGAGGTGGTCCA  120

Qy    891 GAAGTGTAAAAATACAAAAAGTGAGATCCAGGGAGAAGTGCCACCAAGATCAAGGATATC  950
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GAAGTGTAAAAATACAAAAAGTGAGATCCAGGGAGAAGTGCCACCAAGATCAAGGATATC  180

Qy    951 TGTGCCAATTAAAAGGAATGCTATATTGCATAGAAATGAAGTGAGACCACCAGCTCGAGC 1010
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTGCCAATTAAAAGGAATGCTATATTGCATAGAAATGAAGTGAGACCACCAGCTCGAGC  240

Qy   1011 CCAGAAGGCCAGATCTATAAAAATGATAGAAAGACCCAAAATTGCTGCTGCTCGTGGACA 1070
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCAGAAGGCCAGATCTATAAAAATGATAGAAAGACCCAAAATTGCTGCTGCTCGTGTGACA  300

Qy   1071 TTATGATTATTATGTCAACTTGAGGAGTGATGATGGATGTGAGGGAGAAGCACCAAGTTA 1130
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ORIGIN

Query Match   29.3%; Score 602; DB 6; Length 1632;

Best Local Similarity   98.4%;   Pred. No. 7.6e-131;
Matches 608; Conservative   0; Mismatches 10; Indels   0; Gaps   0;

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Qy    264 CATGAAAAGGATCAATAGACAACGGGGTGTGTTATTTAGTGAAGATCAGATCCTCGGTTG 323
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Qy    324 GTTTGTACAGATTCTCTAGGACTAAAACATATTCATGACAGGAAGATATTACACAGGGA 383
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Qy    384 CATAAAAGCTCAGAACATTTTCTTAGCAAGAACCGAATGGTGGCAAAGCTTGGGGACTT 443
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Db    381 CATAAAAGCTCAGAACATTTTCTTAGCAAGAACCGAATGGTGGCAAAGCTTGGGGACTT 440

Qy    444 TGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTTGCTCGAACTTGTATTGGAACACC 503
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Qy    624 CTTACAGCAGCTGGTTCTGGTTGTCAAGCACATTTGCCCCAATATCTCCGGGGTT 683
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Db    621 CTTACAGCAGCTGGTTCTGGTTGTCAAGCACATTTGCCCCAATATCTCCGGGGTT 680

Qy    684 TTCCGTGAGCTCCATTCCTTGATATCTCAGCTCTTCAAGTATCTCCTCGAGACCGACC 743
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Db    681 TTCCCGTGAGCTCCATTCCTTGATATCTCAGCTCTTCAAGTATCTCCTCGAGACCGACC 740

Qy    744 ATCCATAAATTCCATTTTGAAAAGGCCCTTTTTAGAGAATCTTATTCCCAAATATTTGAC 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    741 ATCCATAAATTCCATTTTGAAAAGGCCCTTTTTTAGAGAGATCTTATTCCCAAATATTTGAC 800

Qy    804 TCCTGAGGTCATTCAGGA 821
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Db    801 TCCTGAGGTAAGTTTTGA 818
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RESULT 14
BC053516
LOCUS   BC053516   2281 bp   mRNA   linear   ROD 07-OCT-2003
DEFINITION Mus musculus expressed sequence BB049667, mRNA (cDNA clone
            MGC:54821 IMAGE:6311513), complete cds.
ACCESSION   BC053516
VERSION   BC053516.1 GI:31565169
KEYWORDS   MGC.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 2281)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   MEDLINE   22388257
    PUBMED   12477932
REFERENCE   2 (bases 1 to 2281)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (09-JUN-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Susan L. Sullivan, PhD.
            cDNA Library Preparation: ResGen, Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstron-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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            Young,A., Zhang,L.-H. and Green,E.D.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 100 Row: d Column: 16
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis, similarity but not identity to protein.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="Olfactory epithelium, neonatal mouse,
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                     /clone_lib="NIH_MGC_129"
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                     AGTPYLSPEICQNRPYNNKTDIWSLGCVLYELCTIKHPFESNNFHHLVLKICQGRVA
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```

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          LDKCIEEDTVQENEAVDKLNATLSFEDGTKFQEIRCKEHEDYTDRAFELCGPEAE
          GFFQDVIAAENRRQWDAGAPHTLLRIMAMADVTSTCPTMPDDQVIVMEGSVENGKQW
          WLDVPGTPCALIAAECACSGSLSASKGETVMIKPQLPKEDQBKVEIATGIMVDDEQLEP
          GSDEDIKFPESEDELRSEIIESLEKLAASTEEAQAPSSSKNAEBPGEKEKTNLPVK
          KLQ"
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Below the protein sequence:

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misc_feature   87. .842
               /gene="BB049667"
               /note="S_TKc; Region: Serine/Threonine protein kinases,
               catalytic domain"
               /db_xref="CDD:smart00220"

ORIGIN
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Query Match       29.0%;   Score 595.4;  DB 10;  Length 2281;
Best Local Similarity  81.0%;   Pred. No. 2.7e-129;
Matches  722;  Conservative  0;  Mismatches 156;  Indels  13;  Gaps  2;
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Qy    1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGGAAAGCATACTTA 60
          ||||||||||  |||||| |||||||||| |||||||||||  |||| |||||||||||||
Db   78 ATGGATAACTTTCACCTGATTAAGATCATTGGGGAAGGCACCTTTGGGGAAGGTGTACTTG 137

Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 120
          || |||||||||||||||| ||||| ||||||||||||||||||||   ||  |||||
Db  138 GCTAAAGATAAATCAGAAGCAGTCACTGTGTCATAAAAGAATCAGTTTGACAAAG---  194

Qy  121 CCCATACAAGAGAAAAGAGAGCTTCAAAGAGAAGTGATTCTTCTGGAAAAGATGAAACAT 180
          ||||||   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  195 -------GAAAAGAGGCCTCAAAGAACGAAGTGATTCTTCTCGTGGCTAGGATGGAGCAT 245

Qy  181 CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGAGGAATGGCAGCGGCTGTTATTGTAATG 240
          |||||||||||  ||| |||| |||| || |||||||||||||||||| ||||||||||||
Db  246 CCCAATATCGTAACCTTCTTCAGCTCGTTTCAAGAGCAACGGCCAGGCTGTTGTTATTGTAATG 305

Qy  241 GAATATTGTGATGGAGGGGATCCATGAAAAGGATCAATAGAGAACACGGGTGTGTTATTT 300
          |||| || |||| ||||||||| ||||| ||||||||||||||||||||||||||| |||
Db  306 GAATACTGTGATGGAGGGGATCCCATGCAGAGGATCAGTCCAGAGGCAGCAGCGGGGAGTGATGTTC 365

Qy  301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360
          |||| |||||||||||||||| ||| |||||||||||||||||||| |||||||||||||
Db  366 AGCCAAGAGACCAGATCCTCGTGTTCGTTTGTACACAGATTTCTCTAGGACTGAAGCATATTCAT 425

Qy  361 GACAGGAGAGATATTACACAGGGACATATAAGCTCAGAACATTTTCTCAGCAAGAACGGA 420
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Db  426 GACAGGAGAGATTTTACACAGGGACATTTAGACTCAGATAATTTTCTTAGCAAGAATGGA 485

Qy  421 ATGGTGGCAAAGCTTGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
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Db  486 ATGGTTGCCAAGCTCGGGGACTTTGGAACAGCAAGAGTACTTCCATGGAACTT 545

Qy  481 GCTCGAACTTGTATTGGAACAACCTTACTACCTTGGCTTGGAATATCGTCAGAATAAACCC 540
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Db  546 GCTCCAACATGTGCTGGGACACCTTACCTACCTGTCCCCAGAGATCGTCAGAACAGGCCA 605

Qy  541 TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT 600
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Db  606 TACAACAATAAAACGGACATTTGGTCTCTTGGCTGTGTGTCTTATATGAGCTCTGCCACACTC 665

Qy  601 AAACATCCTTTTGAGGGTAACAACTTACAGAGATTGTTGTCAAGCACAT 660
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Db  666 AAGCATCCTTTTGAGAGTGCAACAACTTCCACCATCCGGTTCTCGAAGATTGTTGTCAAGGACGT 725

Qy  661 TTTGCCCCAATATCTCCGGGGGTTTTCTCGTGAGCTCCATTCCTTGATCATCCAGCTCTTT 720
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Db  726 GTTGCTCCCAATATCACCCCACTTCTCTCGTGACCTCCAGTACCTTGATCACCTCAGCTTTC 785

Qy  721 CAAGTATCTCCCGAGACCGACCATCCATAAATTCCATTTTGAAAAGGCCCTTTTTAGAG 780
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Db  786 AGAGTGTCCCTCCAGGACCGGCCATCCGTTACGTCCCCTTTTTGAAAAGACCCCTTTTAGAA 845

Qy  781 AATCTTATTCCCAAAATATTTGACTCCTGAGGTC-ATTCAGGAAGAGAATTCAGTCACATGCT 839
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Db  846 ACTCTCATTGCCGATCCTGTGATCCTGAGGTGTTCGAGGTCGTTCAAGAAGAGAATTCCAGTCCCACGCT 905
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Qy  840 TATATGCAAGACAAGAGCGCCAGCTTCTCGACATGCTCGGGAAGGTGGTCCA 890
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RESULT 15
BC068201
LOCUS       BC068201   1745 bp   mRNA   linear   PRI 31-MAR-2004
DEFINITION  Homo sapiens cDNA clone IMAGE:4771714, partial cds.
ACCESSION   BC068201
VERSION     BC068201.1  GI:45872598
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1745)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
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            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
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  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1745)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
            Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
            Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhu,
            Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
            Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
            Schein, Asim Siddiqui, Rob Holt, Marco Marra.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 51 Row: k Column: 4
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis.
FEATURES             Location/Qualifiers
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                /lab_host="DH10B"
                /note="Vector: pDNR-LIB"

ORIGIN

Query Match       17.9%;     Score 368;  DB 9;   Length 1745;
Best Local Similarity   66.0%;    Pred. No. 9.6e-76;
Matches 549;    Conservative    0;    Mismatches 280;    Indels    3;    Gaps    1;

Qy     1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTCGGGAAAAGCATACTTA 60
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Qy    61 GCTAAAGGGAAATCAGATAGCAAGCACTCGTGTCATAAAGAGATCAATTTTGAAAAGATG 120
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Db   599 GTTAAATCTACAGAAGATGGCAGACAGTATGTTATCAAGGAAATTAACATCTCAAGAATG 658

Qy   121 CCCATACAAGAAAAAGAGAGCTTCAAAGAAAGAAGAGTGATTCTTCTGGAAAAGATGAAACAT 180
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Db   659 TCCAGTAAAGAAAGAGAGAATCAAGGAGGAAGAGTTGCAGTATTGGCAAACATGAAGCAT 718

Qy   181 CCCAACATTGTAGCCTTCTTCAATTCATTCATTCAAGAGAATGGCAGGCTGTTTATTGTAATG 240
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Db   719 CCAAATATTGTCCAGTATAGAGAATCATTTGAAGAAAATGGCTCTCTCTACATAGTAATG 778

Qy   241 GAATATTGTGATGGAGGGGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAAACATATTCAT 300
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Qy   301 AGTGAAGATCAGATCCTCGGTTGGTTGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360
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Qy   421 ATGGTGGCAAAGCTTGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
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Qy   481 GCTCGAACTTGTATTGGAACACACTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCC 540
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Db  1016 GCTCGAACTTGCCATAGGGACCCCATACTACTTGTCCACCTGAAAATCGTGAAAACAAACCT 1075

Qy   541 TACACACAATAAAACGGATATTTGGCTCGTCCTTCGGCTGCCGTGTCTTATATGAGCTCTGCACACTT 600
         || |  ||| || ||| | |||||  | || | | | ||
Db  1076 TACAATAATAAAAGTGACATTTGGGCTCTCTGGGTGTGTCCTTTATGAGCTGTGTACACTT 1135

Qy   601 AAACATCCTTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACAT 660
         |||  |  ||||| ||||||  |   || |||  |  | | ||  |  |  || | || |
Db  1136 AAACATGCTTTTGAAGCTGGCAGTACTGCAGTGAAAAACCTGGTACTGAAGATATATCTGGATCT 1195

Qy   661 TTTGCCCAATATCTCCGGGGTTTTCTCGTGAGCTGAGTCCATTCCTTGAATATCCTCAGCTCTTT 720
         | | ||| |  ||||| |   ||| ||||| ||||| | || | ||||  ||  || ||||| |
Db  1196 TTTCCACCTGTCTTTGCATTATTCCATGATCCTCCGGATCTCAACTTTGGTGTCTCAGTTATTT 1255

Qy   721 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTTGAAAAGGCCCTTTTTAGAG 780
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Db  1256 AAAAGAAATCCTAGGGATAGAACCATCAGTCAACTCCATATTGGAGAAAGGTTTTTATAGCC 1315

Qy   781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAAATTCAGTC 832
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Db  1316 AAACGCATTGAAAAGTTTCTCTCTCCTCAGCTTATTGCAGAAGAATTTTGTC 1367

Search completed: October 10, 2004, 08:45:53
Job time : 13977 secs
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              GenCore version 5.1.6
         Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October 10, 2004, 03:49:26  ; Search time 229 Seconds
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Title:          US-09-940-921B-1
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Sequence:       1 atggataagtacgatgtgat.........cagtgtcatcctgatgtga 2052

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters:       1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                         SUMMARIES
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Result No.	Score	Query Match	DB	Length	ID	Description
1	1654	80.6	4	2370	US-09-873-404-1	Sequence 1, Appli
2	1654	80.6	4	2370	US-10-243-735-1	Sequence 1, Appli
3	368	17.9	4	5448	US-09-620-312D-246	Sequence 246, App
4	368	17.9	4	5532	US-09-620-312D-245	Sequence 245, App
5	352	17.2	4	4263	US-09-166-350-29	Sequence 29, Appl
6	238.4	11.6	4	1846	US-09-173-581-15	Sequence 15, Appl
7	238.4	11.6	3	1846	US-09-420-915-15	Sequence 15, Appl
8	205.2	10.0	4	63588	US-09-873-404-3	Sequence 3, Appli
9	205.2	10.0	4	63588	US-10-243-735-3	Sequence 3, Appli
10	170.2	8.3	4	2079	US-09-992-481-1	Sequence 1, Appli
11	166.8	8.1	4	2940	US-08-870-529-1	Sequence 1, Appli
12	166.8	8.1	4	2940	US-09-544-794-1	Sequence 1, Appli
13	166.8	8.1	3	3264	US-08-870-529-8	Sequence 8, Appli
14	166.8	8.1	3	3264	US-09-544-794-8	Sequence 8, Appli
15	131.6	6.4	4	1449	US-10-196-927-3	Sequence 3, Appli
16	131.6	6.4	4	1938	US-10-196-927-1	Sequence 1, Appli
17	131.6	6.4	4	2847	US-10-196-927-5	Sequence 5, Appl
18	119.6	5.8	4	2765	US-09-799-451-50	Sequence 50, Appl
19	108.6	5.3	4	2119	US-09-167-206-1	Sequence 1, Appli
20	106.8	5.2	3	906	US-09-221-235-3	Sequence 3, Appli
21	106.8	5.2	3	906	US-09-221-928-3	Sequence 3, Appli
22	106.8	5.2	3	906	US-09-221-527-3	Sequence 3, Appli
23	106.8	5.2	3	906	US-09-221-236-3	Sequence 3, Appli
24	106.8	5.2	3	906	US-09-221-416-3	Sequence 3, Appli
25	106.8	5.2	3	906	US-09-221-245-3	Sequence 3, Appli
26	106.8	5.2	3	906	US-09-163-115-3	Sequence 3, Appli
27	106.8	5.2	3	906	US-09-221-528-3	Sequence 3, Appli
28	106.8	5.2	3	906	US-09-593-553-3	Sequence 3, Appli
29	106.8	5.2	3	906	US-09-221-237-3	Sequence 3, Appli
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31	106.8	5.2	3	4137	US-09-221-235-1	Sequence 1, Appli
32	106.8	5.2	3	4137	US-09-221-928-1	Sequence 1, Appli
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41	106.8	5.2	4	4137	US-09-757-982-1	Sequence 1, Appli
42	100	4.9	4	1060	US-09-579-664B-2	Sequence 2, Appli
43	100	4.9	4	1060	US-10-355-975A-2	Sequence 2, Appli
44	88.6	4.3	1	7218	US-08-232-463-14	Sequence 14, Appl
45	85.2	4.2	3	4880	US-09-031-563-1	Sequence 1, Appli

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                         ALIGNMENTS

RESULT 1
US-09-873-404-1
; Sequence 1, Application US/09873404
; Patent No. 6500656
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL001212-CIP
;  CURRENT APPLICATION NUMBER: US/09/873,404
;  CURRENT FILING DATE: 2001-06-05
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 2370
;  TYPE: DNA
;  ORGANISM: Human
US-09-873-404-1

Query Match             80.6%;  Score 1654;  DB 4;  Length 2370;
Best Local Similarity   94.5%;  Pred. No. 0;
Matches 1763;  Conservative   0;  Mismatches  10;  Indels  93;  Gaps  1;

Qy          1 ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGCCAAGGTGCCTTCGGGAAAGCATACTTA 60
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Db         12 ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGCCAAGGTGCCTTCGGGAAAGCATACTTA 71

Qy         61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 131

Qy        121 CCCATACAAGAAAAGAAGAGCTTCAAAGAAGAAGTGATTCTTCTGGAAAGATGAAACAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 CCCATACAAGAAAAGAAGAGCTTCAAAGAAGAAGTGATTCTTCTGGAAAGATGAAACAT 191

Qy        181 CCCACACATTGTAGCCTTCCTTCATTCATTCAAGAGAATGGCAGGCTGTTTATTGTAATG 240
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Db        192 CCCACACATTGTAGCCTTCCTTCATTCATTCAAGAGAATGGCAGGCTGTTTATTGTAATG 251

Qy        241 GAATATTGTGATGGAGGGGATCCATGAAAAGATCAATAGACAACGGGGTGTGTTATTT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 GAATATTGTGATGGAGGGGATCCATGAAAAGATCAATAGACAACGGGGTGTGTTATTT 311

Qy        301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360
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Db        312 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 371

Qy        361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
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Qy  1561  GCACCTGTGCGAGGACATTGAAGACTTGAAAAAGACTTCAGAACACAAAGGAA  1620
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Qy  1621  AGTAAAAATCCAGAACAGAAATATAAAGCTAAGAGGGGTAAAATTGAAATTAATTTA  1680
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Qy  1681  GACAAATGTATTTCTGATGAAAAACATCCTCCAAGAGGAGGAGGAGGCAATGATATACCAAAT  1740
Db  1599  GACAAATGTATTTCTGATGAAAAACATCCTCCAAGAGGAGGAGGGCAATGATATACCAAAT  1658
Qy  1741  GAAACTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATGATGTGAAAGGAGCAT  1800
Db  1659  GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATGATGTGAAAGGAGCAT  1718
Qy  1801  GGAGATTATACAGACAAAGCATTTGAAAAAACTTCACTGCCCAGAAGCAGGGTTTTCCACG  1860
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Qy  1861  CAGACT  1866
Db  1779  CTGACT  1784
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RESULT 2
US-10-243-735-1
; Sequence 1, Application US/10243735
; Patent No. 6706510
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001212DIV
; CURRENT APPLICATION NUMBER: US/10/243,735
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2370
;   TYPE: DNA
;   ORGANISM: Human
US-10-243-735-1

Query Match   80.6%;   Score 1654;   DB 4;   Length 2370;
Best Local Similarity   94.5%;   Pred. No. 0;
Matches 1763;   Conservative   0;   Mismatches   10;   Indels   10;   Gaps   1;

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Qy     1  ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTA    60
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Qy   121  CCCATACAAGAAAAAGAAGCTTCAAAGAAGAAGATGAGTGATTCTTCGGAAAGATGAAAACAT   180
Db   132  CCCATACAAGAAAAAGAAGCTTCAAAGAAGAAGATGAGTGATTCTTCGGAAAGATGAAAACAT   191
Qy   181  CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGAGATGGCAGGCTGCTGTTATTGTAATG   240
Db   192  CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGAGATGGCAGGCTGCTGTTATTGTAATG   251
Qy   241  GAATATTGTGTGATGGAGGGATCTCATGAAAAGATCAATAGAAAGAATCAATAGAGACAACGCGGGTGTGTTATTT   300
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Qy   601  AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGACAT   660
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Qy   721  CAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTTGAAAAGGCCCTTTTTTAGAG   780
Db   732  CAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTTGAAAAGGCCCCTTTTTAGAG   791
Qy   781  AATCTTATTCCCAAATATTTGACTCCTCGAGGTCATTCAGTGGGAGAATTCAGTCACATGCTT   840
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Qy  1321  GAGCTAAGAAGTAATGGAAGCAGCCTAGAATTCCAGGAGCTGCCATTTAGGAAAAACGAA   1380
Db  1332  GAGCTAAGAAGTAATGGAAGCAGCCTAGAATTCCAGGAGCTGCCATTTAGGAAAAACGAA   1391
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Db  1392  ATGAAGGAACACAGGAATATTGGAAGCAGTTAGAGAAGAAATACCGCCAACAGTACCTCAATGAC   1451
Qy  1441  ATGAAAGAATTAGAAAGAAGAAGATGAAGAAGATGAGGAGAACTCAAAAATAAGTCAT   1500
Db  1452  ATGAAAGAATTAGAAAGAAGAAGATGAAGAAGATGAGGAGGATCAATAGAAGAACTCATGAAAAATAAGTCAT   1488
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Qy  361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACACATTTTCTTAGCAAGAACGGA 420
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Db  372 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGACACATTTTCTTAGCAAGAACCGA 431

Qy  421 ATGGTGGCAAAGCTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
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Qy  481 GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCC 540
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Db  492 GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCC 551

Qy  541 TACACAATAAAACGGATATTTGGTCTCTTGGCCTGTGTCTTATATGAGTCTCGCACACTT 600
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Db  552 TACACAATAAAACGGATATTTGGTCTCTTGGCCTGTGTCTTATATGAGTCTCGCACACTT 611

Qy  601 AAACATCCTTTGAGGGTAACAACTTACAGCAGTGGTCTCGAAGATTTGTCAAGCACAT 660
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Db  612 AAACATCCTTTGAGGGTAACAACTTACAGCAGTGGTCTCGAAGATTTGTCAAGCACAT 671

Qy  661 TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720
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Db  672 TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 731

Qy  721 CAAGTATCTCCTCGAGACCGACCATCCAATAAATTCCATTTGAAAAGGCCCTTTTTAGAG 780
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Db  732 CAAGTATCTCCTCGAGACCGACCATCCAATAAATTCCATTTGAAAAGGCCCTTTTTAGAG 791

Qy  781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGCAAGAATTCAGTCACATGCTT 840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  792 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGCAAGAATTCAGTCACATGCTT 851

Qy  841 ATATGCAGAGCAGGAGCGCCAGCTTCTCGACATGCTGGGAAAGTGGTCCAGAAGTGTAAA 900
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Db  852 ATATGCAGAGCAGGAGCGCCAGCTTCTCGACATGCTGGGAAAGTGGTCCAGAAGTGTAAA 911

Qy  901 ATACAAAAAGTGAGATTCAAGGAAGTGCCCAAGATCAAGGAGATATCTGTGCCAATT 960
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Db  912 ATACAAAAAGTGAGATTCCGGGGAAGTGCCCACCAAGATCAAGGAGATATCTGTGCCAATT 971

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Db 1032 AGATCTATAAAAATGATAGAAGACCCAAATTGCTGCTGTCTGTCTGGACATTATGATTAT 1091

Qy 1081 TATTATGCTCAACTTGATATGCTGGAGTTGAGGAGAGCCCACAAACCAAGTTATCACCCTATT 1140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1092 TATTATGCTCAACTTGATATGCTGGAGTTGAGGAGAGCCCACAAACCAAGTTATCACCCTATT 1151

Qy 1141 CCTCAAGAAAAATAACTGGAGTTGAGGATTACGGTCAGGAACGAGGCCATGGTCCATCCCCA 1200
        |||||||||| || |||||||||||||||||||||||||||| |||||||||||||||||||
Db 1152 CCTCAAGAAAAATAACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCCATGGTCCATCCCCA 1211

Qy 1201 AGTCAATGGCCTGCTACTTCAGAGAAAATTGAAGCTCAACAATAAGTTGAAA 1260
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Db 1212 AGTCAATGGCCTGCTACTTCAGAGAAAATTGAAGCTCAACAATAAGTTGAAA 1271

Qy 1261 GTGGAGAAGCAATGGTCTTGGTCTTCGTCCATCTTCTGCCAGCCAAATTACAACCAGAGACAA 1320
        |||||||||||||||||| |||||||||||||||||||| |||||||||||||||||||||||
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Qy 1321 GAGCTAAGAAGTAATGGAGAAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAAAAACGAA 1380
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Db 1332 GAGCTAAGAAGTAATGGAGAAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAAAAACGAA 1391
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Qy 1381 ATGAAGGAACAGGAGATATTGGAAGCAGTTAGAGGAGAAATACGCCAACAGTACCACAATGAC 1440
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Db 1392 ATGAAGGAACAGGAGATATTGGAAGCAGTTAGAGGAGAAATACGCCAACAGTACCTCAATGAC 1451

Qy 1441 ATGAAAGAAATTAGAAGAAGATGGGGAGAGAACCAGAGAGAACTCAAAAATAAGTCAT 1488
        ||||||||||||||| | ||| ||| |||||||| |||||||
Db 1452 ATGAAAGAAATTAGAAAGAAGAAGAATAGGGGGAGAGACCAG------ 1488

Qy 1501 AAAACCTATTTGGTGAAGAAGAGTAACCTGCGTCCATCAAGCATGTCATCTGAGGAGAGA 1560
Db 1489 ------ 1488

Qy 1561 GCACCTGTCAGGACACATTGAAAAAGACTTGAAACAAATGAGGCTTCGAACAACAAAAGAA 1620
                 |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1489 ------AGGACATTGAAAAAGACTTGAAACAAATGAGGCTTCGAACAACAAAAGAA 1538

Qy 1621 AGTAAAAATCCAGAACACAGAAATATAAAACTAAGAAGGGGTAAAATTTGAAATTAATTTA 1680
        ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db 1539 AGTAAAAATCCAGAACACAGAAATATAAAAGCTAAGAAGGGGGTAAAATTTGAAATTAATTTA 1598

Qy 1681 GACAAATGTATTTCTGATGAAAACATCCTCCAAGAGAGGAATGCAATGATATACCAAAT 1740
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1599 GACAAATGTATTTCTGATGAAAACATCCTCCAAGAGAGGAATGCAATGATATACCAAAT 1658

Qy 1741 GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGAAATGTGTAAAGGAGCAT 1800
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1659 GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGAAATGTGTAAAGGAGCAT 1718

Qy 1801 GGAGATTATACAGACAAAGCAATTGAAAAACTTCACTGCCCCAAGAAGCAGCATTTACAGAA 1860
        ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1719 GGAGATTATACACAGACAAAGCAATTGAAAAACTTCACTGCCCCAAGAAGCAGCATTTACAGAA 1778

Qy 1861 CAGACT 1866
        | |||
Db 1779 CTGACT 1784
```

RESULT 3
US-09-620-312D-246
; Sequence 246, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 246
; LENGTH: 5448
; TYPE: DNA

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;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (534)..(4178)
US-09-620-312D-246

Query Match          17.9%;   Score 368;   DB 4;   Length 5448;
Best Local Similarity  66.0%;  Pred. No. 1.1e-98;
Matches  549;  Conservative  0;  Mismatches 280;  Indels   3;  Gaps   1;

Qy      1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTA 60
            |||||||    ||||||| ||||    |||||||| ||||||   ||| |||||   ||
Db    534 ATGGAGAAGTATGTTAGACTACAGAAGATTGGAGAAGGTTCATTTGGAAAAGCCATTCTT 593

Qy     61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG 120
            ||||     ||||||| |||||  |||||| |||||||   |||| ||| |||  |||
Db    594 GTTAAATCTACAGAAGAGATGGCAGCAGTATGTTATCAAGGAGAAATTAACATCTCAAGAAATG 653

Qy    121 CCCATACAAGAAAAAGAAGCTTCAAAGAAGAGTGATTCTTCTGGAAAAGATGAAACAT 180
            |||  |||    || ||| |||| |||| | ||  |||||||| |||| |||||| ||
Db    654 TCCAGTAAAGAAAGAGAAGAATCAAGGAGAGAAGTTCGAGTATTGGCAAACATGAAGCAT 713

Qy    181 CCCAACATTGTAGCCTTCTTCAATTCATTCAGAGAAGGATCAATAGACAACGGGGTGTGTTATTT 240
            ||  ||| | ||||| | ||||||     ||||| ||| ||||||  |||   || ||||||
Db    714 CCAGTAAAGATCAGTTCCAGTATAGAGAATCATTTGAAGAAAATGGCTCTCTCTACATAGTAATG 773

Qy    241 GAATATTGTGATGGAGGGGATCCTCGGTTGGTTGTTACAGATAGACAATAGAGAGGTGTTATTT 300
            |||  || |||||||||||||||| ||||||||||| ||||||   || | |||||| ||||
Db    774 GATTACTGTGAGGGAGGGGATCCTGTTTAAGCGAATGTTTGCCCTGAAACATGTACAT 833

Qy    301 AGTGAAGATCAGATCCTCCGGTTGGTTGTTTGTACAGATTTTCTCTAGGACTAAAACATATTCAT 360
            |||||||||||||||| ||||||||||| |||||||   ||||| ||||||| |||||| ||||
Db    834 CAAGAGATCAGATTTGGACTGGTTTGTTTGTACAGATATGTTGCCCTGAAACATGTACAT 893

Qy    361 GACAGGAAGATATTACACAGGGACATAAAGCTCAGAACATTTTTCTTAGCAAGAACGGA 420
            |||| ||| ||||||||||||| ||||||||||||||| ||||||||| |||||||||
Db    894 GATAGAGAAAATTCTTCACACAGGGACATTAAAGCTCAGAACATATTTTTAAACTAAGGA 953

Qy    421 ATGGTGGCAAAGCTTGGGACTTTGGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
            |||    |||||||||||||||||   || ||||||||||| |||||||| ||| || ||
Db    954 ACAGT----ACAACTTGGAGATTTGGAATTGCTAGAGTACTGTAATAGTACTGTAGAGCTG 1010

Qy    481 GCTCGAACTTGTATTGGAACACCTTACTACTTCTCCGAGAGATCGTCCCCAGAGAATAAACCC 540
            |||||||||||| |||||||||||||||||||||| |||||||||| ||| ||||||||||||
Db   1011 GCTCGAACTTGCATAGGGACCCCATACTACTTGTCACCTGAAATCTGTGAAAACAAACCT 1070

Qy    541 TACAACAATAAAACGGATATTTGGTCTCTTTTGCTGTGTCTTATATGAGAGCTCTGCACACTT 600
            ||||| ||||||   |||||||||| | | |||||||| || |||||||||||||||||||||
Db   1071 TACAATAATAAAAGTGATGCATTTGGGTGTCTCGGGTGTGGTGTCCTTTATGAGCTGTGTACACTT 1130

Qy    601 CAAGTATCTCCTCGAGACCGACCCATCCATAAATTCCATTTTTGAAAAGGCCCTTTTTAGCC 660
            ||||||||||| |||||||| ||| |||| ||||| |||||||| |||||||||| ||||
Db   1131 TACAATAAAGCTTTGAGGTAACAACTTACAGACCTGGTTACTGGCAGTATGATATCTGGATCT 1190

Qy    661 AAAGAAATCCTAGGATAGACCAATCAACTCAACTCAGTCAACTCAGAGAATTCAGTC 720
            ||||| ||||  || | ||||||||||||| |||| |||||||| || ||||||||
Db   1191 TTTGCCCAATATCTCCGGGGGTTTCTCTGAGCTCCATTCCTGATCTCCAGCTCTTT 1250

Qy    721 CAAGTATCTCCTCGAGACCGACCATAGAGCCAATCCTATTAGGGAGAAAAGGCCCTTTTATGAGAG 780
            ||||| | ||||||||||||| || |||| ||||  ||| |||| |||| | ||||||| |||||
Db   1251 CAAGTGTCGGGATCGTGATGAGTCGTTAAGCGAATGTTTAAGCATCAGAATGCTGTTATTT 1310

Qy    781 AATCTTATTCCCAAATATTTGACTTCATTGACTTCAGGAGGAATTCAGTC 832
            |||||||  |||||  ||||| | ||||||| |||| |||||||||||||
Db   1311 AAACGCATTGAAAAGTTTCTCTCCTCCCCAGCTGTTCTGCTGCTGTTCAGAGAAGAATTTTTGTC 1362
```

```
RESULT 4
US-09-620-312D-245
;  Sequence 245, Application US/09620312D
;  Patent No. 6569662
;  GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
```

;   APPLICANT: Liu, Chenghua
;   APPLICANT: Asundi, Vinod
;   APPLICANT: Zhang, Jie
;   APPLICANT: Ren, Feiyan
;   APPLICANT: Chen, Rui-hong
;   APPLICANT: Zhao, Qing A.
;   APPLICANT: Wehrman, Tom
;   APPLICANT: Xue, Aidong J.
;   APPLICANT: Yang, Yonghong
;   APPLICANT: Wang, Jian-Rui
;   APPLICANT: Zhou, Ping
;   APPLICANT: Ma, Yunqing
;   APPLICANT: Wang, Dunrui
;   APPLICANT: Wang, Zhiwei
;   APPLICANT: John Tillinghast
;   APPLICANT: Drmanac, Radoje T.

```
;   TITLE OF INVENTION: No. 6569662del Nucleic Acids and
;   TITLE OF INVENTION: Polypeptides
;   FILE REFERENCE: 784CIP2B
;   CURRENT APPLICATION NUMBER: US/09/620,312D
;   CURRENT FILING DATE: 2000-07-19
;   PRIOR APPLICATION NUMBER: 09/552,317
;   PRIOR FILING DATE: 2000-04-25
;   PRIOR APPLICATION NUMBER: 09/488,725
;   PRIOR FILING DATE: 2000-01-21
;   NUMBER OF SEQ ID NOS: 1105
;   SOFTWARE: pt_FL_genes Version 1.0
;
SEQ ID NO 245
;   LENGTH: 5532
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (534)..(4262)
US-09-620-312D-245

Query Match          17.9%;   Score 368;   DB 4;   Length 5532;
Best Local Similarity  66.0%;  Pred. No. 1.1e-98;
Matches  549;  Conservative  0;  Mismatches 280;  Indels   3;  Gaps   1;

Qy      1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTA 60
            |||||||    ||||||| ||||    |||||||| ||||||   ||| |||||   ||
Db    534 ATGGAGAAGTATGTTAGACTACAGAAGATTGGAGAAGGTTCATTTGGAAAAGCCATTCTT 593

Qy     61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG 120
            ||||     ||||||| |||||  |||||| |||||||   |||| ||| |||  |||
Db    594 GTTAAATCTACAGAAGAGATGGCAGCAGTATGTTATCAAGGAGAAATTAACATCTCAAGAATG 653

Qy    121 CCCATACAAGAAAAAGAAGCTTCAAAGAAGAGTGATTCTTCTGGAAAAGATGAAACAT 180
            |||  |||    || ||| |||| |||| | ||  |||||||| |||| |||||| ||
Db    654 TCCAGTAAAGAAAGAGAAGAATCAAGGAGAGAAGTTCGAGTATTGGCAAACATGAAGCAT 713

Qy    181 CCCAACATTGTAGCCTTCTTCAATTCATTCAGAGAAGGATCAATAGACAACGGGGTGTGTTATTT 240
            ||  ||| | ||||| | ||||||     ||||| ||| ||||||  |||   || ||||||
Db    714 CCAGTAAAGATCAGTTCCAGTATAGAGAATCATTTGAAGAAAATGGCTCTCTCTACATAGTAATG 773

Qy    241 GAATATTGTGATGGAGGGGATCCTCGGTTGGTTGTTACAGATAGACAATAGAGAGGACGGA 300
            |||  || |||||||||||||||| ||||||||||| ||||||   || | |||||| ||||
Db    774 GATTACTGTGAGGGAGGGGATCCTGTTTAAGCGAATGTTTGCCCTGAAACATGTACAT 833

Qy    301 AGTGAAGATCAGATCCTCCGGTTGGTTGTTTGTACAGATTTTCTCTAGGACTAAAACATATTCAT 360
            |||||||||||||||| ||||||||||| |||||||   ||||| ||||||| |||||| ||||
Db    834 CAAGAGATCAGATTTGGACTGGTTTGTTTGTACAGATATGTTGCCCTGAAACATGTACAT 893

Qy    361 GACAGGAAGATATTACACAGGGACATAAAGCTCAGAACATTTTTCTTAGCAAGAACGGA 420
            |||| ||| ||||||||||||| ||||||||||||||| ||||||||| |||||||||
Db    894 GATAGAGAAAATTCTTCAGAGAGTCCTGATAGAGCTCCGGATAAATGCTCAGAAATGCTCTAGGACTAAATGCTCCTAGGACATATGTTTTACAGATAAGATGGA 953

Qy    421 ATGGATGAAGATCAGATGAGATTTTGGTGTACAGGGATCTCCGGTTGGTTGTTTGTATTT 480
            ||||| |||||||||||| ||||||||| || |||  |||| ||||| ||||||| |||
Db    954 ATGGGTGATGATGAGATTCAATGGGATCATCATGATGAAAAGATCAATAGAGACACAACGGG 1010

Qy    481 GCTCGAACTTGTATTGGAACACCTTACTACTTCTCCGAGAGATCGTCCCCAGAGAATAAACCC 540
            |||||||||||| |||||||||||||||||||||| |||||||||| ||| ||||||||||||
Db   1011 ACAGT--ACAACTTGGAATTGCTAGAGTTCTTAATAGTACTGTAGAGCTG 1010
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Db  1011 GCTCGAACTTGCATAGGGACCCCATACTACTTGTCACCTGAAATCTGTGAAACAAACCT 1070
         ||||||||||| ||  |||||||  || ||||||||||||| ||||||||||||| |||||
Qy   541 TACAACAATAAAACGGATATTTGGTCTCTGTCTTATATGAGCTCTGCACACTT 600

Db  1071 TACAATAATAAAAGTGACATTTGGGCTCTGGGGTGTGTCCTTTATGAGCTGTGTACACTT 1130
Qy   601 AAACATCCTTTTGAGGGTAACAACTTACAGCAGCACTGGTCTCGAAGATTGTCAAGCACAT 660

Db  1131 AAACATGCTTTTGAGCTGCAGTATGAAAAACCTGGTACTGAAGATAATCTGGATCT 1190
Qy   661 TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCTTGATAATCTCAGCTCTT 720

Db  1191 TTTCCACCTGTGTCTTTGCATTATTCCATGATCTCCCAGTTTGGTGTCTCAGTTATTT 1250
Qy   721 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTAGAG 780

Db  1251 AAAAGAAATCCTAGGGATAGACCATCAGTCAACTCCATATTGGAGAAAGGTTTTTATAGCC 1310
Qy   781 AATCTTATTCCCAAATATTGACTCCTGAGGTCATTCAGGAAGAATTCAGTC 832

Db  1311 AAACGCATTGAAAAGTTTCTCTCTCCCAGCTTATTGCAAGAAGAATTTTGTC 1362
```

RESULT 5
US-09-166-350-29
; Sequence 29, Application US/09166350A
; Patent No. 6440663
GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; TITLE OF INVENTION: Uses Therefor
; FILE REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 4263
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-166-350-29

Query Match   17.2%;   Score 352;   DB 4;   Length 4263;
Best Local Similarity   64.8%;   Pred. No. 5.4e-94;
Matches 539;   Conservative   0;   Mismatches 290;   Indels   3;   Gaps   1;

```
Qy     1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGGCATACTTA 60
Db   576 ATGGAGAAGTATGTGAGACTGCGCAAGCACTGTGTCATAAAAGAGATCAATTTGAAAGATG 635

Qy    61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG 120
Db   636 GTTAAATCGACAGAGGATCGGCAGACATTATTGTCATCAAGCAGAAAATTAACATCTCAAGGAATG 695

Qy   121 CCCATACAAGAGAAAAAGAAGCTTCAAAGAAGAAGAGAGTGATTCTTCTGGAAAAGATGAAACAT 180
Db   696 TCTGATAAAGAAAAGGCAAGAATCAAGGAGAGGAAGTTGCGTATTGGCAAACATGAAGCAT 755

Qy   181 CCCAACACATTGTAGCTTCTTCAATTCAATTCATTTCAAGAGAATGGCGAGGCTGTTTATTGTAATG 240
Db   756 CCAAATATTGTCCAATATAAAGAATCATTTGAAGAAAATGGCTTCTCTACATAGTAATG 815

Qy   241 GAATATTGTGATGGAGGGGAATCATCATGAAAGGATCAATAGACAACGGGGTGTGTTATTT 300
Db   816 GATTACTGCGAGAGGAAGGTGATTGTTGTTTAAACGAATAAATGTCTTAAAATGCTGACTAGTAATG 875
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Db   301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360
Qy   876 CAAGAAGACCAGATTTTGGACTGGTTTGTGTGCAGATATGTTGGCTCTGAAGCATGTACAT 935

Db   361 GACAGGAAGATATTACCAGGGACTAAAAGTCAGAACATTTTCTTAGCAAGAACCGA 420
Qy   936 GATAGAAAAATTCTTCACCGAGAACATAAAGTCACAGAACATATTTCTAACCAAAGATGGG 995

Db   421 ATGGTGGCAAAGCTGGGAACTTGGTATAGCAAGAGCTCCTGAATAATTCCATGGAACTT 480
Qy   996 ACAGTG---CAGCTTGGAGATTTGAAGTTGCTCGAGTTCTTAATAGTACTGTAGAGCTG 1052

Db   481 GCTCGAACTTGTATTGAACACCTTACCTACTTGTCCCCAGAGATCTGTCAGAATAAACCC 540
Qy  1053 GCTCGAACTTGCATAGGGCACTCCATACTACTTGTCACCTGAAATCTGTGAAAACAAGCCT 1112

Db   541 TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTGTGCTTATGAGCTCTGCACACTT 600
Qy  1113 TATAACAATAAAAGTGACATTTGGGCTTTGGGCTGTGTGTCCTTTATGAGTTGTGTACACTT 1172

Db   601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCGAAGATTGTCAAGCACAT 660
Qy  1173 AAACATGCATTGAAGCTGCAGTATGAACATGAAAAACCTGGTACTGAAGATAATCTCCGGATCC 1232

Db   661 TTTGCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCTTGATAATCTCAGCTCTTT 720
Qy  1233 TTTCCTCCAGTGTCTCCACCATTACTCCTATGATCTCCCAGCTTGCTTGCTCTCCAGTTATTT 1292

Db   721 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTAGAG 780
Qy  1293 AAAAGAAATCCTAGGGATAGACCATCAGTCAACTCCATATTGGAGAAAGGTTTTTATAGCT 1352

Db   781 AATCTTATTCCCAAATATTGACTCCTGAGGTCATTCAGGAAGAATTCAGTC 832
Qy  1353 AAACGAATCGAAAAGTTTCTCTCCCTCAGCTTATTGCGAGAAGAATTTTGTC 1404
```

RESULT 6
US-09-173-581-15
; Sequence 15, Application US/09173581A
; Patent No. 6013455
GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzai, Yalda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PF-0614 US
; CURRENT APPLICATION NUMBER: US/09/173,581A
; CURRENT FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 1846
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1567782
US-09-173-581-15

Query Match   11.6%;   Score 238.4;   DB 3;   Length 1846;
Best Local Similarity   67.5%;   Pred. No. 2.1e-60;
Matches 351;   Conservative   0;   Mismatches 166;   Indels   3;   Gaps   1;

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Qy   313 ATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCATGACAGGAAGATA 372
Db   370 ATTTTGGACTGGTTTGTGTACAGATATGTTGGCCCTGAAACATGTTGCGCCCTGAAACATGATGAGAAAATT 429
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Db   430 CTTCATCGAGACATAAATCTCAGAGACACATATTTTAACTAAAGATGGAACAGT--ACAA 486
         |||||                |||||||||||   ||||           ||| |   |||
Qy   433 CTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTTGCTCGAACTTGT 492
         ||||| |  ||||| ||| || || ||| ||||   |  |  |  ||| || ||||||||
Db   487 CTTGGGAGATTTGGAATTGCTAGAGTTCTTAATAGTACTGTAGAGCTGGCTCGAACTTGC 546
Qy   493 ATTGGAACACCTTACTACCTGTCCCAGAGATCGTCAGAATAAACCCTACACACAATAAA  552
         | ||| ||| ||||||||| ||||  ||| |||||||  ||| ||||| ||| |||| ||
Db   547 ATAGGGACCCCATACTACTTGTCACCTGAATCTGTGAAAACAAACCTTACAATAATAA   606
Qy   553 ACGGATATTTGGTCTCTTGGCTGTCTTATATGAGCCTCTGCACACTTAAACATCCTTTT  612
         | ||||||||||| || |||| ||| ||||||||| | |||||||||||||||| ||||
Db   607 AGTGACATTTGGGCTTCGGGGTGTCCTTTATGAGCTGTGTACACTTAAACATGCTTTT   666
Qy   613 GAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACATTTGCCCCAATA  672
         || |  | ||  | |  |       ||||||||||  ||    |||| ||| || |||
Db   667 GAAGCTGGCAGTATGAAAAACCTGGTACTGAAGATAATATCTGGATCTTTTCCACCTGTG 726
Qy   673 TCTCCCGGGGTTTTCTGTGAGCTCCATTCCTGATATCTTCAGCTGTCTTCAGTATCTCCT 732
         ||| ||  | |||  | |||| ||| ||  ||| |||  |||||| | | || ||| ||
Db   727 TCTTTGCATTATTCCTATGATCTCCGCAGTTGTGTCTCCAGTTATTTAAAAGAAATCCT   786
Qy   733 CGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTGAGAGAATCTTATTCCC 792
         | | | | |||| |  | |||| ||| || ||| | | | |||  | ||||  || ||
Db   787 AGGGATAGACCATCAGTCAACTCCATATTGGAGAAAGGTTTATAGCCAAACGCATTGAA  846
Qy   793 AAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTC 832
         ||  | ||| | |  ||| |  ||| |||||||| | |||
Db   847 AAGTTTCTCTCTCTCTCAGCTTATTGCAGAAGAATTTTGTC 886
```

RESULT 8
US-09-873-404-3
; Sequence 3, Application US/09873404
; Patent No. 6500656
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001212-CIP
; CURRENT APPLICATION NUMBER: US/09/873,404
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 63588
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(63588)
; OTHER INFORMATION: n = A,T,C or G
US-09-873-404-3

```
Query Match             10.0%;  Score 205.2;  DB 4;  Length 63588;
Best Local Similarity   96.3%;  Pred. No. 1.6e-49;
Matches   210;  Conservative    0;  Mismatches    8;  Indels    8;  Gaps    0;

Qy     606 TCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACATTTTGC 665
           | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27430 TCAGTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACATTTTGC 27489
Qy     666 CCCAATATCTCCGGGGGTTTTCTGTGAGCTCCATTCCTTGATATCCTTGATATCTCTTTCAAGT 725
           |||||||||||||||| |||||||||||||||||||||| ||||||||||||||||||||||||
Db   27490 CCCAATATCTCCGGGGGTTTTCTGTGAGCTCCATTCCTGAGCTCGTGAGATTCCTGATATCTCAGTCTTTTCAGT 27549
Qy     726 ATCCTCCTGAGACCGACCATCCATCATAAATTCCATTTTGAAAAGGCCCTTTT 785
           |||||||||||||||||||||||||| |||||||||||||||||||||||| |
Db   27550 ATCCTCCTGAGACCGACCGACCATCCATCCATAAATTCCATTTTGAAAAGGCCCTTTTTTAGAGAATCT 27609
Qy     786 TATTCCCAAATATATTTGACTCCTGAGGTCATTCAGGAAG 823
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Qy   373 TTACACAGGGACATAAAAGCTCGAGAACATTTTCTTAGCAAGAACGAATCGTGGCAAAG 432
         |||       |||||||  |||||| |||||   ||         ||  ||| | |||
Db   430 CTTCATCGAGACATAAATCTCAGAGACACATATTTTAACTAAAGATGGAACAGT--ACAA 486
Qy   433 CTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTTGCTCGAACTTGT 492
         ||||| |  ||||| ||| || || ||| ||||   |  |  |  ||| || ||||||||
Db   487 CTTGGGAGATTTGGAATTGCTAGAGTTCTTAATAGTACTGTAGAGCTGGCTCGAACTTGC 546
Qy   493 ATTGGAACACCTTACTACCTGTCCCAGAGATCGTCAGAATAAACCCTACACACAATAAA  552
         | ||| ||| ||||||||| ||||  ||| |||||||  ||| ||||| ||| |||| ||
Db   547 ATAGGGACCCCATACTACTTGTCACCTGAATCTGTGAAAACAAACCTTACAATAATAA   606
Qy   553 ACGGATATTTGGTCTCTTGGCTGTCTTATATGAGCCTCTGCACACTTAAACATCCTTTT  612
         | ||||||||||| || |||| ||| ||||||||| | |||||||||||||||| ||||
Db   607 AGTGACATTTGGGCTTCGGGGTGTCCTTTATGAGCTGTGTACACTTAAACATGCTTTT   666
Qy   613 GAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACATTTGCCCCAATA  672
         || |  | ||  | |  |       ||||||||||  ||    |||| ||| || |||
Db   667 GAAGCTGGCAGTATGAAAAACCTGGTACTGAAGATAATATCTGGATCTTTTCCACCTGTG 726
Qy   673 TCTCCCGGGGTTTTCTGTGAGCTCCATTCCTGATATCTTCAGCTGTCTTCAGTATCTCCT 732
         ||| ||  | |||  | |||| ||| ||  ||| |||  |||||| | | || ||| ||
Db   727 TCTTTGCATTATTCCTATGATCTCCGCAGTTGTGTCTCCAGTTATTTAAAAGAAATCCT   786
Qy   733 CGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTGAGAGAATCTTATTCCC 792
         | | | | |||| |  | |||| ||| || ||| | | | |||  | ||||  || ||
Db   787 AGGGATAGACCATCAGTCAACTCCATATTGGAGAAAGGTTTATAGCCAAACGCATTGAA  846
Qy   793 AAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTC 832
         ||  | ||| | |  ||| |  ||| |||||||| | |||
Db   847 AAGTTTCTCTCTCTCTCAGCTTATTGCAGAAGAATTTTGTC 886
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RESULT 7
US-09-420-915-15
; Sequence 15, Application US/0942091S
; Patent No. 6264947
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzai, Yalda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PF-0614 US
; CURRENT APPLICATION NUMBER: US/09/420,915
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/173,581
; EARLIER FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 1846
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1567782
US-09-420-915-15

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Query Match             11.6%;  Score 238.4;  DB 3;  Length 1846;
Best Local Similarity   67.5%;  Pred. No. 2.1e-60;
Matches   351;  Conservative    0;  Mismatches  166;  Indels    3;  Gaps    1;

Qy   313 ATCCTCCGTTGGTTGTACAGATTTCTTAGGACTAAAACATATTCATGACAGGAAGATA 372
         || |  | ||||||||||||| |  |  |||||| ||||| | ||||| |  |||  |
Db   370 ATTTTGGACTGGTTGTACAGATATATGTTTGGCCCTGAAACATGTACAGAAACATGATAGAAAAATT 429
Qy   373 TTACAGGGGACATAAAAGCTCGAGAACATTTTCTTAGCAAGAACGGAATCGTGGCAAAG 432
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Query Match            8.3%;   Score 170.2;  DB 4;   Length 2079;
Best Local Similarity 52.1%;   Pred. No. 4.5e-40;
Matches 404;  Conservative    0;  Mismatches 368;   Indels    3;   Gaps    1;

Qy      1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCAGGAGTGCCTTCGGCAAGAAAGCATACTTA   60
          ||| |||    |||  || ||  |  || ||||||||    |||  ||||   ||| ||    |
Db      1 ATGGAGAAGTACGAGGCGGATCCGAGTGGTGGGGAGAGTGCCTTCGGGATTGTGCACCTG   60

Qy     61 GCTAAAGGGAAATCAGATAGCAACGCACTGTCATAAAGAGATCAATTTGAAAAGATG  120
          |||  ||| |||   || || ||| |||     ||| || |||| || ||| ||||||
Db     61 TGCCTGCGAAAGGCTGACCAGAGCGTGGTGATCATCAAGCAGATTCCAGTGGACAGATG  120

Qy    121 CCCATACAAGAAAAAGAGAGCTTCAAAGAAAGAAGTGATTCTTCTGGAAAAGATGAAACAT  180
          ||||     ||  ||  ||| ||  ||| ||    |||  ||| || |||| || || |||
Db    121 ACCAAGGAGGAGCGGCGCAGCGAGCAGCCGCAGATGAGTGCCAGGTCCTCAACGCTGCTCAACCAC  180

Qy    181 CCCAACATGTGAGCCTTCTCAATTCATTTCAAGAGAATGGCAGGCGTGTTTATTGTAATG  240
          |||  |  |  |||| | ||||| ||| | |||||||  ||  |||||||| || ||| |
Db    181 CCCAATGTCATTGATACTACGAGAACTTCCTGGAAGACAAAGCCCTTATGATCGACATG  240

Qy    241 GAATATTGTGATGGAGGGGATCTCATGAAAAAGGATCAATAGACAACGGGGTGTGTTATTT  300
          |||| |  |  ||| ||| | | |||
Db    241 GAATATGCACCAGGCGACTTCGGCTGAGTTCATCCAAAAGCGCTGTAATTCCCTGCTG  300

Qy    301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT  360
          |||   ||| |  ||   |     || | ||| || || || ||| |  | || || | |
Db    301 GAGGAGGAGACCATCCTGAGCTTCTCGTCGATCCTGCTTCGCTCCACTGCATCATGTGCAC  360

Qy    361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAGACACATTTTCTTAGCAAGAAACGGA  420
          || ||||| | || ||| | |   | ||||  || |||| ||||  |||| || || |||
Db    361 ACCCACCTCATCCTGCACCGAGACCTCAAGACCCAGACATCCTGCTTGACAAAACACCGC  420

Qy    421 ATGGTGCAAAGCTTGGGGACTTGGATAGCAAGAAGCTCCTGAATAATTCCATGGAACTT  480
          || | |  |||  || || || | || || || |||
Db    421 ATGTCGTCAAGATCGGTGATTTCGGGCATCTCCAAGATCCT---TAGCAGCAAGAGCAAG  477

Qy    481 GCTCGAACTTGTATTGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAAACCC  540
          || || ||| | ||| ||| |||    |||     ||| || | || || || || |||
Db    478 GCCTACACGGTGGTGGGTACCCCATGGTGTCCTCTGAGCTGTGTGGGCAAGCCC  537

Qy    541 TACAACAATAAAAACGGATATTTGGTCTCTTGGTGTCTTATATGAGCTCTGCACACTT  600
          ||||| | | || ||| || ||| |||     || || || ||||| |||| || |||
Db    538 TACAACCAGAAGAGTAGCAGTGACATCGGGGCCGTGTGTCCTCTACGAGGTGGCCAGCCTC  597

Qy    601 AAACATCCTTTTGAGGGTAACAACTTCACAGCAGCTGGTTCTGAAGATTGTCAAGCACAT  660
          |||| |  | |||| ||  || || ||||| | ||||| |||| || || || ||| |||
Db    598 AAGAGGGCTTTCGAGGCTTGCAGAGCCTGCAGACTTGCTGCTGAGATCATGAGTGGCACC  657

Qy    661 TTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGTCTTT  720
          ||||  | ||| || ||  || || || |||| | ||  || ||| || || ||  |||
Db    658 TTTGCACTATCTCTGCACCGGTACGGTACCAGCCCTACAGCCCTTGCCAGCTGGTCCTGAGTCTACTC  717

Qy    721 CAAGTATCCTCCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTT  775
          |||| || ||  || ||| || |||     || || || || |||||||| |
Db    718 AGCCTGGAGCCTGCCCAGTGCCTGCCCACACTCAGCCACCATCATGCGCACAGCCCCCTCT  772
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Db     27610 TATTCCCAAATATTTGACTCCTGAGGTAAGTTTTGAGG  27647
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Query Match           10.0%;   Score 205.2;  DB 4;   Length 63588;
Best Local Similarity 96.3%;   Pred. No. 1.6e-49;
Matches 210;  Conservative    0;  Mismatches    8;   Indels    0;   Gaps    0;

Qy    606 TCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAAGCACATTTTGC  665
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27430 TCAGTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAAGCACATTTTGC  27489

Qy    666 CCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGTCTTTCAAGT  725
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27490 CCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGTCTTTCAAGT  27549

Qy    726 ATCTCCTGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTAGAGAATCT  785
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27550 ATCTCCTGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTAGAGAATCT  27609

Qy    786 TATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAG  823
          ||||||||||||||||||||||||||||||||||||||
Db  27610 TATTCCCAAATATTTGACTCCTGAGGTAAGTTTTGAGG  27647
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STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/870,529
  FILING DATE: 06-JUN-1997
  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
  NAME: McMasters, David D.
  REGISTRATION NUMBER: 33,963
  REFERENCE/DOCKET NUMBER: 480052.418
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (206) 622-4900
  TELEFAX: (206) 682-6031
US-08-870-529-1
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 2940 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  FEATURE:
  NAME/KEY: CDS
  LOCATION: 1..2937
US-08-870-529-1

Query Match           8.1%;    Score 166.8;  DB 3;  Length 2940;
Best Local Similarity 54.8%;   Pred. No. 5.9e-39;
Matches 352;  Conservative  0;  Mismatches 287;  Indels  3;  Gaps  1;

Qy   25 GCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTAGCTAAAGGGAAATCAGATAGCAAG 84
          ||||| |  |||||||||||||||||     |  |||
Db  169 GTCCTGGGCCGCGGCCTTCGGGAGGAAGCCACGCGTGTACCCGCCGACCGGATGACTCA 228

Qy   85 CACTGTGTCATAAAAGAGATCAATTTGAAAAGATGAAACATCCCAACATTTGAGCCTTCTTCAAT 204
          ||||||||
Db  229 CTGGTTGTGTGGAAGGAAGTCGATTTGACCCGGCCTGTCTGAGAAGGAACGTCGTGATGCC 288

Qy  145 AAGAAGAAGTGATTCTTCTGAAAAGATGAAACATCCCAACATTTGAGCCTTCTTCAAT 204
Db  289 TTGAATGAGATAGTTATTCTCGGCACTGCTGCAGCACGACAACATTATTGCCTACTACAAT 348

Qy  205 TCATTTCAAGAGAATGGCAGGCGTGTTATTGTAATGCAGCTGCTGATTGAGTCTGCAGCAGGGATCTC 264
Db  349 CACTTCATGGACAATACCACGCTGCTGATTGAGTCTGCAGCAGGATCTC 408

Qy  265 ATGAAAAGGATCAATAGACAACCGGGTGTGTTATTTAGTGAAGATCAGATCCTCGGTTGG 324
Db  409 TATGACAAAATCCTTGTGTCAGAGGACAAGAGTGTTGTTGAAGATAGTGGTGTGGTAC 468

Qy  325 TTTGTACAGATTTCTCTAGGACTAAAACATATTCATGCAAGAACGGAATGTGGCAAGTTGGGGACTTT 444
Db  469 CTATTTCAGATTGTTTCAGCAGTGAGCTGCATCCATAAAGCTGCAATCCTTCATAGAGAT 528

Qy  385 ATAAAAGCTCAGAACATTTTTCTGAATAATTCCATGGAACTTGCTCGAACTTGTGATTTGGGGACACCT 504
Db  529 ATAAAGACATTAAATATTTTTCTGACCAAG--GCAAAACCTGATAAAACTTGGAGATTAT 585

Qy  445 GGTATAGCAAGAGTCCTGAATAATTCCATGGAACTTGCTCGAACTTGTATTGGAACACCT 504
Db  586 GGCCTAGCAAGAAACTTAATTCTGAGTATTCCATGGCTGAGAGCGCTGAGAGCGATATTTGG 645

Qy  505 TACTACCTGTCCCCAGAGATCTGTGCTCTTATATGAGCCTGCACACTTAAAACATCCTTTTGAGGGTAACAAC 624
Db  646 TATTACATGTCTCCAGAGCTTCCTCAAGGAGTAAAGTACAATTTCAAGTCTGTATCTGG 705

Qy  565 TCTCCTTGGCTGTGTCTTTATATGAGCCTGCACACTTAAAACATCCTTTTGAGGGTAACAAC 624
Db  706 GCAGTTGGCTGCTGCTGCTCATTTTTGAACTGCTTGACCTGCTTTGGACCACCTCGGAC 765
```

```
RESULT 12
US-09-544-794-1
; Sequence 1, Application US/09544794
; Patent No. 6541232
; GENERAL INFORMATION:
;   APPLICANT: Sims, John E.
;   APPLICANT: Virca, G. Duke
;   APPLICANT: Bird, Timothy A.
;   APPLICANT: Anderson, Dirk M.
;   TITLE OF INVENTION: Polypeptides Having Kinase Activity
;   FILE REFERENCE: 2005-B
;   CURRENT APPLICATION NUMBER: US/09/544,794
;   CURRENT FILING DATE: 2000-04-07
;   PRIOR APPLICATION NUMBER: 08/870,529
;   PRIOR FILING DATE: 1997-06-06
;   PRIOR APPLICATION NUMBER: 60/059,979
;   PRIOR FILING DATE: 1996-06-10
;   NUMBER OF SEQ ID NOS: 18
;   SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 1
;   LENGTH: 2940
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2940)
US-09-544-794-1

Query Match           8.1%;    Score 166.8;  DB 4;  Length 2940;
Best Local Similarity 54.8%;   Pred. No. 5.9e-39;
Matches 352;  Conservative  0;  Mismatches 287;  Indels  3;  Gaps  1;

Qy   25 GCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTAGCTAAAGGGAAATCAGATAGCAAG 84
Db  169 GTCCTGGGCCGCGGCCTTCGGGAGGAAGCCACGCGTGTACCCGCCGACCGGATGACTCA 228

Qy   85 CACTGTGTCATAAAAGAGATCAATTTGAAAAGATGCCATACAAGAAAAAGAAGCTTCA 144
Db  229 CTGGTTGTGTGGAAGGAAGTCGATTTGACCCGGCCTGTCTGAGAAGGAACGTCGTGATGCC 288

Qy  145 AAGAAGAAGTGATTCTTCTGAAAAGATGAAACATCCCAACATTTGAGCCTTCTTCAAT 204
Db  289 TTGAATGAGATAGTTATTCTCGGCACTGCTGCAGCACGACAACATTATTGCCTACTACAAT 348

Qy  205 TCATTTCAAGAGAATGGCAGGCTGTGTTATTGTAATGCAGCTGCTCC 264
Db  349 CACTTCATGGACAATACCACGCTGCTGATTGAGTCTGCAGCAGGATCTC 408

Qy  265 ATGAAAAGGATCAATCAATAGACAACGGGGTGTGTTATTTAGTGAAGATCAGATCCTCGGTTGG 324
Db  409 TATGACAAAATCCTTCGTCAGAGGACAAGCAGTTGTTGAAGATAGTGGTGTGGTAC 468

Qy  325 TTTGTACAGATTTCCTAGGACTAAAACATATTTCATGCAAGAACGGAATGTGGCAAGTTTGGGGACTTT 444
Db  469 CTATTTCAGATTGTTTCAGCAGTGAGCTGCATCCATAAAGCTGCAATCCTTCATAGAGAT 528

Qy  385 ATAAAAGCTCAGACATTTTTCTGAATAATTCCATGGAACTTGCTCGAACTTGTGGGGACTTT 504
Db  529 ATAAAGACATTAAATATTTTTCTGACCAAG--GCAAAACCTGATAAAACTTGGAGATTAT 585

Qy  445 GGTATAGCAAGAGTCCTCAGATCGTCGAGATAAACCCTACAACAATAAAACGGATATTTGG 504
Db  586 GGCCTAGCAAGAAACTTAATTCTGAGTATTCCATGGCTGAGAGCGCTGAGAGCGATATTTGG 645

Qy  505 TACTACCTGTCCCCAGAGATCTGTCAGAGAATAAACCCTTTTGAGGGTAACAAC 564
Db  646 TATTACATGTCTCCAGAGCTTCCTCAAGGAGTAAAGTACAATTTCAAGTCTGTATCTGG 705
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Qy 265 ATGAAAAGGATCAATAGACAACGGGGTGTGTTATTAGTGAAGATCAGATCCTCGGTTGG 324
     |||||||| ||| | ||||| ||||||| ||| | |||||||||| | ||||||
Db 528 TATGACAAAATCCTTCGTCAGAAGACAGAGTTGTTTGAGGAAGGATGGTGGTGTGGTAC 587

Qy 325 TTTGTACAGATTTCTCTAGGACTAAAACATATTCATGACAGGAAGATATTACCAGGGAC 384
     ||| ||||||| || ||||||| | ||| ||| | ||||| ||| | |||||
Db 588 CTATTTCAGATTGTTTCAGCAGTGAGTGCATCCATAAAGCTGGAATCCTTCATAGAGAT 647

Qy 385 ATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGAATGGTGCAAAGCTTGGGGACTTT 444
     ||||| |||||| |||| ||||| |||||| ||||||| | ||||| |||
Db 648 ATAAAGACCATTAAATATTTTTCGACCAAG--GCAAACCTGATAAAACTTGGAGATTAT 704

Qy 445 GGTATAGCAAAGAGTCCTGAATAATTCATGGAACTTGCTCGAACTTGTATTGGAACACCT 504
     ||| ||| |||| | ||| | || || ||||| | ||||| || |||
Db 705 GGCCTAGCAAAGAGAACTTAAATTCTGAGTATTCCATGGCTGAGACGGCCTTGTGGGAACCCCA 764

Qy 505 TACTACCTGTCCCCAGAGATCTGTCAGAGATCTGTCAGAATAAACCCTACAACAATAAAACGGATATTTGG 564
     ||||| | | | ||||| | | |||| ||| | || ||||
Db 765 TATTACATGTCTCCAGAGCTCTGTCAGCAGGAGTAAAGTACAATTTCAAGTACCTGATATCTGG 824

Qy 565 TCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTTAAACATCCTTTGAGGGTAACAAC 624
     ||||||||| | || || ||| | | |||| || |||||||| ||
Db 825 GCAGTTGGCTGCGTCATTTTGAACTGCTTACCTTAAAGAGGACGTTTGATGCTACAAAC 884

Qy 625 TTACAGCAGCTGGTTCTGAAGATTGTCAAGCACATTTTGCC 666
     |||| | |||| ||| |||| | ||| ||| ||
Db 885 CCACTTAACCTGTGTGGAGATCGTGCAAGGAATTCGGGCC 926

RESULT 14
US-09-544-794-8
; Sequence 8, Application US/09544794
; Patent No. 6541232
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: Polypeptides Having Kinase Activity
; FILE REFERENCE: 2005-B
; CURRENT APPLICATION NUMBER: US/09/544,794
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 08/870,529
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/059,979
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 3264
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-794-8

Query Match 8.1%; Score 166.8; DB 4; Length 3264;
Best Local Similarity 54.8%; Pred. No. 6.3e-39;
Matches 352; Conservative 0; Mismatches 287; Indels 3; Gaps 1;

Qy 25 GCCATCGGGCAAGGTGCCTTCGGGAAGCATACTTAGCTAAAGGGAAATCAGATAGCAAG 84
    || ||||| || ||| ||| |||||| | ||||| ||||
Db 288 GTCCTGGGCGCCGCGCCCTTCGGGGAAGCCACCGTGTACCGCCGCCGAGGATGACTCA 347

Qy 85 CACTGTGTCATAAAAGAGATCAATTTGAAAAGATGCCATACAAGAAAAAGAAGCTTCA 144
    || | ||| |||||| | ||| ||| |||| | || |||| ||||| ||
Db 348 CTGGTTGTGTGGAAGGAAGTCGATTTGACCCCGGCTGTCTGAGAAGGACGTCGTGATGCC 407

Qy 145 AAGAAAGAAGTGATTCTTCTGGAAAAGATGAAACATCCCAACATTGTAGCCTTCTTCAAT 204
    |||| ||||| ||| || | ||||| | || ||| | ||| ||
Db 408 TTGAATGAGATAGTTATTCTGCAGCACTGCTGTTATTGTAATGGAATATTGTGATGGAGGGGATCTC 467

Qy 205 TCATTTCAAGAGAATGGCAGGCTGTGTTATTGTAATGGAATATTGTGATCGAGGGGATCTC 264
    || ||| | || |||| | | || ||| | | || ||||
Db 468 CACTTCATGGACAATACCACCGCTGCTGATTGAGCTGGAATATTGTAATGAGGAGGAACCTG 527

Qy 265 ATGAAAAGGATCAATAGACAACGGGGTGTGTATTTAGTGAAGATCAGATCCTCGGTTGG 324
Db 528 TATGACAAAATCCTTCGTCAGAAGACAAGTTGTTTGAGGAGAGATGGTGTGTGTGTAC 587

Qy 325 TTTGTACAGATTTCTCTAGGACTAAAACATATTCATGACAGGAAGATATTACACAGGGAC 384
Db 588 CTATTTCAGATTGTTTCAGCAGTGAGCTGCATCCATAAAGCTGGAATCCTTCATAGAGAT 647

Qy 385 ATAAAAGTCAGACACATTAAATATTTTTCTTCTTCAGCAGAACGGAATGGTGCCAAAGCTTGGGGACTTT 444
Db 648 ATAAAGACATTAAATATTTTTCTGACCAAG--GCAAACCTGATAAAACTTGGAGATTAT 704

Qy 445 GGTATAGCAAGAGTCCTGAATAATTCCATGGAACTTGCTCGAACTTGTGATTGGAACACCT 504
Db 705 GGCCTAGCAAGAAACTTAATTCTGAGTATTCCATGGTATGCGACGGTGAGACCCCCA 764

Qy 505 TACTACCTGTCCCCAGAGATCGTGTCAGAATAAACCCTACAACAATAAAACGATATTGG 564
Db 765 TATTACATGTCTCCAGAGCTCTGTCAAGGAGTAAAGTACAATTTCAAGTCTGATATCTGG 824

Qy 565 TCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTTAAACATCCTTTGAGGGTAACAAC 624
Db 825 GCAGTTGGCTGCTGCTCATTTTTGAACTGCTGCTTACCTTAAAGAGAGCGTTGATGCTACAAAC 884

Qy 625 TTACAGCAGCTGTTCTGAAGATTTGTCAAGCACATTTGCC 666
Db 885 CCACTTAACCTGTGTGTGAAGATCGTGCAAGGAGGAATTCGGGGCC 926

Db 415 TTTATCCAGCTGCTGCTGGGAGTTGACTACATGCATGAGAGGAGGATACTTCATCGAGAC 474
Qy 385 ATAAAAGTCAGAACATTTTTCTTCTTAGCAAGAACGGAATGGTGGCAAAGCTTGGGGACTTT 444

Db 475 TTAAAGTCAAAGAATGTATTTCTGAAAAATAA-----TCTCCTTAAAATTGGAGATTTT 528
Qy 445 GGTATAGCAAGAGTCCTGAATAATTCCATGGAACTTGCTCGAACTTGTGATTGGAACACCT 504

Db 529 GGAGTTTCTGCACTTCTAATGGGATCCTGTGACCTGGCCACAACTTTAACTGGAACTCCC 588
Qy 505 TACTACCTGTCCCCAGAGATCGTGTCAGAATAAAACCTACAACAATAAAACGGATATTTGG 564

Db 589 CATTATATGAGTCCTGAGGCTCTGAAACACCAAGGCTATGACACAAAGTCGGAACATCTGG 648
Qy 565 TCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTTAAACATCCTTTGAGGGTAACAAC 624

Db 649 TCACTGGCATGCATGTGGTCTGAAGATTGTCAAGCACATTTGCCCCAATATCTCCGGGTT 708
Qy 625 TTACAGCAGCTGGTTCTGAAGATTGTCAAGCACATTTGCCCCAATATCTCCGGGGTT 684

Db 709 TTCTTATCCATTGTTTAAAAATTGTGAGGTGACACACTTCTCTCCCTGAGAGATAT 768
Qy 685 TCTCGTGAGCTCCATTCCTGATATCTCAGCTCTTCAGTATCCTCGAGATCCTGAGACCGACCA 744

Db 769 CCAAAAGAACTAAATGCCATCATGGAAAGCATGTTGAACAAGAATCCTTCATTAAGACCA 828
Qy 745 TCCATAAATTCCATTTGAAAAGGCCCTTTTAGAGAATCTTATTCCCAA 794

Db 829 TCTGCTCATCGAAATTTAAAAATCCCTTACCTTACCTTGATGAGCGAGCTACAGAA 878

Search completed: October 10, 2004, 08:49:42
Job time : 234 secs

RESULT 15
US-10-196-927-3
; Sequence 3, Application US/10196927
; Patent No. 6797510
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6797510el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0348-USA
; CURRENT APPLICATION NUMBER: US/10/196,927
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/293,248
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1449
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-196-927-3

Query Match 6.4%; Score 131.6; DB 4; Length 1449;
Best Local Similarity 51.3%; Pred. No. 1.1e-28;
Matches 364; Conservative 0; Mismatches 334; Indels 12; Gaps 2;

Qy 91 GTCATAAAAGAGAGATCAATTTGAAAAGATGCCCATACAAGAAAAAGAAGCTTCAAAGAAA 150
Db 175 GTACTTAAGGAAATATCTGTTGGAGAACTAAATCCAATGAAACTGTACAGGCCCAATTTG 234

Qy 151 GAAGTGATTCTTCTGAAAAAGATGAAACATCCCAACATTGTAGCCTTCTTCAATTCATTT 210
Db 235 GAAGCCCAACTCCCTCCAAGCTGGACCACCCAGCCATTGTCAAGTTCCATGCAAGTTTT 294

Qy 211 CAAGAGAATGGCAGGCGTGTTTATTGTAATGGAATATTGTGATGGAGGGGATCTCATGAAA 270
Db 295 GTGGAGCAAGATAATTTCTGCATTATCACGGAGTACTGTGAGGGGCCGAGATCTGGACGAT 354

Qy 271 AGGATCA-----ATAGACAACGGGGTGTGTTATTTAGTGAAGATCAGATCCTCGGTTGG 324
Db 355 AAAATTCAGGAATATAAACAAGCTGGAAAAATCTTTCCAGAAAAATCAAATAATAGAATGG 414

Qy 325 TTTGTACAGATTTCTCTAGGACTAAAACATATTCATGACAGGAAGATATTACACAGGGAC 384

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 03:49:50 ; Search time 9615 Seconds
                                        (without alignments)
                                        7776.841 Million cell updates/sec

Title: US-09-940-92lB-1
Perfect score: 2052
Sequence: 1 atggataagtacgatgtgat........cagtgctcatcctgatgtga 2052
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:
                1: gb_est1:*
                2: gb_est2:*
                3: gb_htc:*
                4: gb_est3:*
                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_gss1:*
                9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1209	58.9	1483	3	CR598570	CR598570 full-leng
2	c	843.8	41.1	890	5	BX350584	BX350584 BX350584
3		814.6	39.7	980	5	BX342707	BX342707 BX342707
4		595.4	29.0	1434	3	AK054168	AK054168 Mus muscu
5		595.4	29.0	2407	3	AK032672	AK032672 Mus muscu
6		594	28.9	603	9	AY405588	AY405588 Homo sapi
7		576.4	28.1	872	5	BX417448	BX417448 BX417448
8		536.8	26.2	670	6	CD700193	CD700193 EST16717
9		514.8	25.1	928	5	BQ917635	BQ917635 AGENCOURT
10		474	23.1	856	6	CD243608	CD243608 AGENCOURT
11		464.8	22.7	603	9	AY405589	AY405589 Pan trogl
12		455.4	22.2	603	9	AY405590	AY405590 Mus muscu
13		452.4	22.0	659	2	BB666328	BB666328 BB666328
14		447.8	21.8	678	5	BX328262	BX328262 BX328262
15		390	19.0	639	2	BB623078	BB623078 BB623078
16		389.6	19.0	643	2	BB665975	BB665975 BB665975
17		368	17.9	1628	3	BC015147	BC015147 Homo sapi
18		361.6	17.6	857	7	CN158710	CN158710 947521 MA
19		352	17.2	2070	3	AK031330	AK031330 Mus muscu
20		352	17.2	5362	3	BC070443	BC070443 Mus muscu
21		350.4	17.1	3568	3	AK077047	AK077047 Mus muscu
22		343.2	16.7	3103	3	AK034754	AK034754 Mus muscu
23		328.4	16.0	648	4	BJ061491	BJ061491 BJ061491
24		320.2	15.6	904	5	BX369829	BX369829 BX369829

25		313.4	15.3	732	7	CN531454	CN531454 UI-M-HOO-
26		309.6	15.1	706	6	CD802687	CD802687 UI-M-GVO-
27		306.6	14.9	630	6	BJ029013	BJ029013 BJ029013
28		293.8	14.3	718	6	CB312741	CB312741 AGENCOURT
29		274.2	13.4	700	7	CF531621	CF531621 UI-M-FY0-
30		265.2	12.9	2465	5	AK045202	AK045202 Mus muscu
31	c	260	12.7	498	5	BX342706	BX342706 BX342706
32	c	259.4	12.6	763	7	CN160628	CN160628 949825 MA
33		254.2	12.4	649	6	CD291255	CD291255 StrPu538.
34		252.2	12.3	493	2	AW988570	AW988570 ug10a11.y
35		248.2	12.1	812	5	BU322582	BU322582 603849586
36		247.4	12.1	860	5	BP142906	BP142906 BP142906
37		242.8	11.8	913	5	BQ431111	BQ431111 AGENCOURT
38		241	11.7	908	5	BX375816	BX375816 BX375816
39		240.6	11.7	730	7	CN531024	CN531024 UI-M-HOO-
40		240.2	11.7	927	5	BU516066	BU516066 AGENCOURT
41		238	11.6	930	5	BX364188	BX364188 BX364188
42		238	11.6	1835	3	CR606903	CR606903 full-leng
43		237.6	11.6	1971	3	CR612915	CR612915 full-leng
44		237.4	11.6	907	6	CA790699	CA790699 AGENCOURT
45		236	11.5	819	6	CF285034	CF285034 AGENCOURT

ALIGNMENTS

RESULT 1
CR598570

LOCUS   CR598570   1483 bp   mRNA   linear   HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DL005YK18 of B cells (Ramos cell line)
            Cot 25-normalized of Homo sapiens (human).
ACCESSION   CR598570
VERSION   CR598570.1 GI:50479377
KEYWORDS   HTC; CNSLT cDNA.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1483)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK   Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
            Faraday Avenue
REFERENCE   2 (bases 1 to 1483)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES   Location/Qualifiers
     source   1..1483
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DL005YK18"
                     /tissue_type="B cells (Ramos cell line) Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

Query Match   58.9%; Score 1209; DB 3; Length 1483;
Best Local Similarity   100.0%; Pred. 2.9e-297;
Matches 1209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGGCAAGTGCCTTCGGGAAAGCATACTTA 60
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Db   94 ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGGCAAGTGCCTTCGGGAAAGCATACTTA 153

Qy 1141 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAGAAACGAGCGAGGCATGGTCCATCCCCA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1234 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAGAAACGAGCGAGGCATGGTCCATCCCCA 1293

Qy 1201 AGTCAATGG 1209
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Db 1294 AGTCAATGG 1302

RESULT 2
BX350584/c
LOCUS   BX350584   890 bp   mRNA   linear   EST 23-APR-2004
DEFINITION BX350584 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL005YK18 3-PRIME, mRNA sequence.
ACCESSION   BX350584
VERSION   BX350584.1 GI:30379530
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 890)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            6942.r,
            and it belongs to a clone representative of this cluster. For more
            information about this cluster and the virtual cDNA, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAI043ZA11_1&c=6942.r
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DL005YK18"
                     /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                     /cell_line="RAMOS CELL LINE"
                     /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                     25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match   41.1%; Score 843.8; DB 5; Length 890;
Best Local Similarity 98.3%; Pred. No. 4.7e-204;
Matches 873; Conservative   0; Mismatches 13; Indels   2; Gaps 2;

Qy   254 GAGGGGATCTCATGAAAGATCAATAGACAACGGGGTGTGTTATTAGTGAAGATCAGA 313
          ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   890 GAGGGGATCTCATGAAAGATCAATAGACAACGGGGTGTGTG-TATTAAGTGAAGATCAGA 832

Qy   314 TCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCATGACAACGAAGATAT 373
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   831 TCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCATGACAACGAAGATATT 772

Qy   374 TACACAGGGACATAAAAGTCAGAACATTTTCTTAGCAAGAACGGATGGTGGCAAAGC 433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   771 TACACAGGGACATAAAAGTCAGAACATTTTCTTAGCAAGAACGGATGGTGGCAAAGC 712

Qy   434 TTGGGGACTTTGGTATAGCAAGAGAGTTCCTGAATAATTCCATGAACAAGAATTCCGAACTTGTA 493
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   61 GCTAAAGGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 GCTAAAGGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 213

Qy   121 CCCATACAGAAAAAGAGAGCTTCAAAGAAAGAAGTGATTCTTCTGGAAAGAATGAAACAT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 CCCATACAGAAAAAGAGAGCTTCAAAGAAAGAAGTGATTCTTCTGGAAAGAATGAAACAT 273

Qy   181 CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAGAATGGCAGGTGTTATTGTAATG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAGAATGGCAGGTGTTATTGTAATG 333

Qy   241 GAATATTGTGATGGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTATTT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334 GAATATTGTGATGGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTATTT 393

Qy   301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 453

Qy   361 GACAGGAAGATATTACACAGGGACATAAAAGTCAGAACATTTTCTTAGCAAGAACGGA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   454 GACAGGAAGATATTACACAGGGACATAAAAGTCAGAACATTTTCTTAGCAAGAACGGA 513

Qy   421 ATGGTGGCAAAGTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGAACTT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   514 ATGGTGGCAAAGTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGAACTT 573

Qy   481 GCTCGAACTTGTTGAACACACTTACCTACCTGTCCCCAGAGATCTGTCGAATAAACCC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   574 GCTCGAACTTGTTGAACACACTTACCTACCTGTCCCCAGAGATCTGTCGAATAAACCC 633

Qy   541 TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTCTGTGTCTTATATGAGCTCGCACACTT 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   634 TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTCTGTGTCTTATATGAGCTCGCACACTT 693

Qy   601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAAGCACAT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   694 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAAGCACAT 753

Qy   661 TTTGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   754 TTTGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 813

Qy   721 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCCTTTTTAGAG 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   814 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCCTTTTTAGAG 873

Qy   781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   874 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT 933

Qy   841 ATATGCAGACAGGAGCCGCCAGCTTCCCGACATGCTGGGAAGTGGTCCAGAAGTGTAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   934 ATATGCAGACAGGAGCCGCCAGCTTCCCGACATGCTGGGAAGTGGTCCAGAAGTGTAAA 993

Qy   901 ATACAAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATATCTGTGCCAATT 960
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Db   994 ATACAAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATATCTGTGCCAATT 1053

Qy   961 AAAAGGAATGCTATATTGCATAGAAATGAATGAAATGCTGTGTCGTGTGGACATTAGATTAT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1054 AAAAGGAATGCTATATTGCATAGAAATGAATGAAATGCTGTGTCGTGTGGACATTAGATTAT 1113

Qy 1021 AGATCTATAAAAATGATAGAAAGACCCAAAATTGCTGCGTGTCGTGTCGTGGACATTATGATTAT 1080
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Db 1114 AGATCTATAAAAATGATAGAAAGACCCAAAATTGCTGCGTGTCGTGTCGTGGACATTATGATTAT 1173

Qy 1081 TATTATGCTCAACTTGATATGCTGAGGAGAGCCCACAAACCAAGTTATCACCCTATT 1140
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Db 1174 TATTATGCTCAACTTGATATGCTGAGGAGAGCCCACAAACCAAGTTATCACCCTATT 1233

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Db    711  TTGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTTGTA 652
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Qy    494  TTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGATAAACCCTACAACAATAAAA 553
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db    651  TTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGATAAACCCTACAACAATAAAA 592

Qy    554  CGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTTAAACATCCTTTTG 613
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db    591  CGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTTAAACATCCTTTTG 532

Qy    614  AGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAAGCACATTTGCCCCAATAT 673
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db    531  AGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAAGCACACATTTGCCCCAATAT 472

Qy    674  CTCCGGGGTTTCTGTGAGCTCCATTCCTGATATCTCAGCTCTTCAAGTATCTCCTC 733
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db    471  CTCCGGGGTTTCTCGTGAGCTCCATTCCTGATATCTCAGCTCTTCAAGTATCTCCTC 412

Qy    734  GAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTAGAGAATCTTATTCCCA 793
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db    411  GAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTAGAGAATCTTATTCCCA 352

Qy    794  AATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTTATATGCAGAGCAG 853
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db    351  AATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTTATATGCAGAGCAG 292

Qy    854  GAGCGCCCAGCTTCTCGACATGCTGGGGAAGTGGTCCAGAAGTGTAAAATACAAAAGTGA 913
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db    291  GAGCGCCCAGCTTCTCGACATGCTGGGGAAGTGGTCCAGAAGTGTAAAATACAAAAGTGA 232

Qy    914  GATTCCAGGGAAAGTGCCCACCAAGATCAAGAGATATCTGTGCCAATTAAAAGGAATGCTA 973
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Db    231  GATTCCAGGGAAAGTGCCCACCAAGATCAAGAGATATCTGTGCCAATTAAAAGGAATGCTA 172

Qy    974  TATTGCATAGAAATGAATGAGAGACCACCAGCTGAGCGTGGAGGCCAGATCTATAAAAA 1033
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db    171  TATTGCATAGAAATGAATGAGAGACCACCAGCTGAGCGTGGAGGCCAGATCTATAAAAA 112

Qy   1034  TGATAGAAGAAGACCCAAAAATTGCTGTCGTGTGTGGACATTATGATTATTATTGCTCAAC 1093
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db    111  TGATAGAAGAAGACCCAAAAATTGCTGTCGTGTGTGGACATTATGATTATTATTGCTCAAC 52

Qy   1094  TTGATATGCTGAGGAGGAGGCCCACAAACCAAGTTATCACCCTATTC 1141
               ||||||||||| |||||||||||||||||||||||||||||
Db     51  TTGATATGCT-AGGAGGAGGAGGCCCACAAACCAAGTTATCACCCATTTC 5
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RESULT 3

BX342707

LOCUS   BX342707   980 bp   mRNA   linear   EST 08-APR-2004

DEFINITION BX342707 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL005YK18 5-PRIME, mRNA sequence.

ACCESSION   BX342707

VERSION   BX342707.2   GI:46279550

KEYWORDS   EST.

SOURCE   Homo sapiens (human)

ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 980)

AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE   Full-length cDNA libraries and normalization

JOURNAL   Unpublished (2001)

COMMENT   On May 2, 2003 this sequence version replaced gi:30344086.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
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6942.r,
and it belongs to a clone representative of this cluster. For more
information about this cluster and the virtual cDNA, see
http://www.genoscope.cns.fr/cdna?s=CS0DL005BF09QP1&c=6942.r.
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FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CS0DL005YK18"
                     /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                     /cell_line="RAMOS CELL LINE"
                     /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                     25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match   39.7%;   Score 814.6;   DB 5;   Length 980;
Best Local Similarity   97.7%;   Pred. No. 1.4e-196;
Matches 863;   Conservative 5;   Mismatches 9;   Indels 6;   Gaps 4;

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Qy      1  ATGGATAAGTACAGATGTGATTAAG-GCCATCGGGCAAGGTGCCTCGGGAAAGCATACTT 59
               |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db     94  ATGGATAAGTACAGATGTGATTAAGCGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTT 153

Qy     60  AGCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGAT 119
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154  AGCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGAT 213

Qy    120  GCCCATACAAGAAAAAGAGAGCTTCAAAGAAGAAGTGATTCTTCTGGAAAAGATGAAACA 179
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214  GCCCATACAAGAAAAAGAGAGCTTCAAAGAAGAAGTGATTCTTCTGGAAAAGATGAAACA 273

Qy    180  TCCCAACATTGTGCCTTCTTCTTCAATTCATTCAATTCATTCAAGAGAATGGCAGGCTGT 239
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274  TCCCAACATTGTGAGCCTTCTTCTTCAATTCATTCAATTCAAGAGAATGGCAGGCTGT 333

Qy    240  GGAATATTGTGATGGAGGGGATCCATGAAAAGGATCAATAGACAACGGGTGTGTTATT 299
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334  GGAATATTGTGATGGAGGGGATCCATGAAAAGGATCAATAGACAACGGGTGTGTTATT 393

Qy    300  TAGTGAAGATCAGATCCTCGGTTGGTTTGTTGTTGTACAGATTTCTTAGCACATATTCA 359
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394  TAGTGAAGATCAGATCCTCGGTTGGTTTGTTGTTGTACAGATTTCTTAGCACATAATTCA 453

Qy    360  TGACAGGAAGATATTACACAGGGACATAAAGCTCAGAACATTTTTCTTAGCAAGAACG 419
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454  TGACAGGAAGATATTACACAGGGACATAAAGCTCAGAACATTTTTCTTAGCAAGAACGG 513

Qy    420  AATGGTGCAAAGCTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACT 479
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514  AATGGTGCAAAGCTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACT 573

Qy    480  TGCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACC 539
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Db    574  TGCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACC 633

Qy    540  CTACAACAATAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACT 599
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634  CTACAACAATAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACT 693

Qy    600  TAAACATCCTTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACA 659
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694  TAAACATCCTTTTGAGGGTAACAACTTACAGCAGCTGGGT-ACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACA 752

Qy    660  TTTTGCCCCAATATCTCCGGGGTTTCTGTGAGCTCCATTCCTTGATATCCTTAGCTCTT 719
               ||||||||||||||||||| |||||||||||||||:||||| |||||||||||||||||
Db    753  TTTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATYCCTGAGCTCCATTTCCAGTCCTT 812

Qy    720  TCAAGTATCTCCTGCGAGACCGACCATCCATAAATTCCATTTTGAAAAGGGCCCTTTTAGA 779
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Db   813  TCAAGTAGTCCCTCGAGACCGACCATCCATAAATTCCATTTTGAAGAGGCCCTTTTTAGA 872
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   780  GAATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCT 839
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   873  GAATCTTATTCCCAAATATTTGACTCCTGRGGTCATTCAGGAAG-ATTCAGTCACATGCT 931
Qy   840  TATATGCAGAGCAGGAGCGCCCAGCTTCTCGACATGCTGGGAAG 882
          |||||||||    ||-|:  :|||||||||||||||||:|:|
Db   932  TATATGCAG--AGAGGAGGSGCASTTCTTCGACATGCTGGRAGG 971
```

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RESULT 4
AK054168
LOCUS       AK054168              1434 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN
            full-length enriched library, clone:E230024I12 product:weakly
            similar to protein kinase nek1 (EC 2.7.1.-) [Mus musculus], full
            insert sequence.
ACCESSION   AK054168
VERSION     AK054168.1  GI:26344040
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE   1
AUTHORS     Carninci,P. and Hayashizaki,Y.
TITLE       High-efficiency full-length cDNA cloning
JOURNAL     Meth. Enzymol. 303, 19-44 (1999)
MEDLINE     99279253
PUBMED      10349636
REFERENCE   2
AUTHORS     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE     20549374
PUBMED      11042159
REFERENCE   3
AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS     The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE       Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1434)
AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,I., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Itoh,M., Kagawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
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COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1..1434
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:E230024I12"
                     /db_xref="taxon:I0090"
                     /clone="E230024I12"
                     /sex="female"
                     /tissue_type="oviduct"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="2 days pregnant adult"
     CDS             104..1114
                     /note="unnamed protein product; putative
                     weakly similar to protein kinase nek1 (EC 2.7.1.-) [Mus
                     musculus] (PIR|S25284, evidence: FASTY, 46.5%ID,
                     54.7%length, match=1247)"
                     /codon_start=1
                     /protein_id="BAC35677.1"
                     /db_xref="GI:26344041"
                     /translation="MDNFHLIKIIGEGTFGKVYLAKDKSESSHCVIKEISLTKEKEAS
                     KNEVILLARMEHPNIVTFSSFQENGRLPIVMEYCDGGDLMQRIQRQRGVMFSEDQIL
                     CWFVQISLGLKHIHDRKILHRDIKSQNIFLSKNGMVAKLGDFGTARTLNDSMELAQTC
                     AGTPYYLSPEICQNRPYNNKTDIWSLGCVLYELCTLKHPFESNNFHHLVKICQGRVA
                     PISPHFSRDLQSLIPQLRVSPQDRSPVTSLLKRPFLETLIARSLYPEVCSRRIQSHA
                     HMENMAIGPTACWRVSPWWDHVTMSLKSMRGWLGVVAVRLPSLHKILPEFHPQCHKNE
                     KF"
ORIGIN
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Qy     1  ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTA 60
          ||||||||||||| |||||| ||||||||| ||||||||||| |||||||| |||||||
Db   104  ATGGATAACTTTCACCTGATTAAGATCATTGGGGAGGCACCTTTGGGAGGTGTACTTG 163

Qy    61  GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   164  GCTAAAGATAAATCAGAAAGCAGTCACTGTGTCATAAAAGAAATCAGTTTGACAAAG--- 220

Qy   121  CCCATACAAGAAAAGAAGCTTCAAAGAAAGAAGTGATTCTTCTGAAAAGATGAAACAT 180
          ||                    |||||||||  ||||||  ||| |||    |||
Db   221  ---------GAAAAAGAGGCCTCAAAGAACGAAGTGATTCTTCTGGCTAGGATGGAGCAT 271

Qy   181  CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGAGAATGGCAGGCTGTTTATTGTAATG 240
          ||||| |  ||||| |||| |||| |||| ||||||||   ||| ||||| ||| |||||
Db   272  CCCAATATCGTAACCTTCTTCAGCTTCAGTTCAAGAGAACCGCAGGCTGTTTATTGTAATG 331

Qy   241  GAATATTGTGATGGAGGGGGATCTCATGAAAAGAATGAAATCAGTTTGACAAAG--- 300
          |||| |||||| |||||| |||||||  ||  ||||  |||   ||| | ||||| |||
Db   332  GAATACTGTGATGGGGGGGATCTCATGCAGAGGATCCAGAGGCAGCGGGGAGTGATGTTC 391
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Qy    301  AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAACATATTCAT  360
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Db    392  AGCGGAAGACCAGATCCGTGTTGGTTGTACAGATTTCTCTAGGACTGAGCATATTCAT   451

Qy    361  GACAGGAAGATATTACACAGGGACAATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA  420
           |||||||  |||||||||||||||  |||||||||||||||||||||||||||||||||
Db    452  GACAGGAAGATTTTACACAGGGACACTAAAATCTCAGAATATTTTCTTAGCAAGAATGGA  511

Qy    421  ATGGTGGCAAAGCTGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT     480
           ||||||  |||||||   ||  ||  |||  ||||||||  |||||||||||||||||
Db    512  ATGGTTGCCAAGCTCGGGGACTTTGGAACAGCAAGAACACTGAATGACTCCATGGAACTT  571

Qy    481  GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCC  540
           |||   ||  ||||  |||||||   |||  ||||||||||||||||  |||||||||
Db    572  GCTCAAACATGTGTGGGACACCTTACTACCTGTCCCCAGAGATCGTGTCAGAACAGGCCA  631

Qy    541  TACACAATAAAAGCGGATATTTGGTCTCCTTGGCGTGTCTTATATGAGCTCTGCACACTT  600
           ||||||||||||  ||||  ||||  ||  ||||||||||  ||||||||||||||||
Db    632  TACACAATAAAAGCGGACATCTGGTCTTTTGGCGTGTCTTATATGAGCTCTGCACACTC   691

Qy    601  AAACATCCTTTTGAGGGTAACAACTTACAGCCAGCTGGTTCGAAGATTTGTCAAGCACAT  660
           |||||||||||||||||   ||||   ||  |||||||||||||||  |||||||||
Db    692  AAGCATCCTTTTGAGAGCAACAACTTCCACCATCCGGTTCTGAAGATTTGTCAAGGACGT  751

Qy    661  TTTGCCCCAATATCTCCGGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTT  720
           ||||   |||||  ||  |||||||  ||  ||||||||||||||||||||||||||
Db    752  GTTGCTCCCATATCACCCCACTTCTCTCGTGACCTACAGTCCTTGATACCTCAGCTCTTC  811

Qy    721  CAAGTATCCTCGACCAGACCGACCATCCATAAATCCATTTGAAAAGGCCCTTTTAGAG   780
           ||||||  |||  ||  |||  ||||||||  |  |||  |||  |||||||||||||
Db    812  AGAGTGTCTCCTCAGGACCGGACCATCCGCCATCCGTCCCTTTGAAAAGACCCCTTTTAGAA  871

Qy    781  AATCTTATTCCCAAATATTTGACTCCTGAGGTC-ATTCAGGAGGAAATTCAGTCACATGCT  839
           |||||||||||  |||||   |||  |||||||||  ||  ||||||||||||||||||
Db    872  ACTCTTCATTGCCCGATCCTTGTATCCTGAGGTCTGTTCAAGAAGAAATCCAGTCCCACGGT  931

Qy    840  TATATGCAGAGCAGGAGCGCCAGGTTCTCGACATGCTGGACATGCTGGTGGTCCAGAAGTGTAA  899
           ||||  |||   |||   ||  ||||  |  ||||  ||||||||||||||||||||||
Db    932  CACATGGAACAATGGCCATTGGCCCCACCAGCTTGTTGTGGAGAGTTAGTCCATGGTGGGGAT  991

Qy    900  AATACAA   906
           ||  ||
Db    992  CATGTAA   998
```

RESULT 5
AK032672

LOCUS   AK032672   2407 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length
            enriched library, clone:6530411J22 product:weakly similar to
            protein kinase nek1 (EC 2.7.1.-) [Mus musculus], full insert
            sequence.
ACCESSION   AK032672
VERSION   AK032672.1 GI:26328482
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   MEDLINE 99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   MEDLINE 20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system-384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   MEDLINE 20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 2407)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,T., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC);
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
            URL:http://fantom.gsc.riken.jp/.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:6530411J22"
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                     /clone="6530411J22"
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                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="10 days neonate"
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                     weakly similar to protein kinase nek1 (EC 2.7.1.-) [Mus
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Db    860  ACTTCTCATTGCCCGATCCTTGTATCCTGAGGTCTTGTTCCAGAAGAATCAGTCCCACGCT  919
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Qy    840  TATATCGAGCAGCAGGAGCGCCAGCTTCCTCGACATGCTGGAAGGTGGTCCA  890
                ||| |  ||| ||           ||||| |||||||||||| |||||
Db    920  CACCATGGAGACAATGCGCCATTGGCCCACCACAGCTTGTTGGAGAGTTAGTCCA  970
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RESULT 6
AY405588
LOCUS        AY405588                603 bp    DNA      linear    GSS 12-DEC-2003
DEFINITION   Homo sapiens HCM2274 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION    AY405588
VERSION      AY405588.1  GI:39761562
KEYWORDS     GSS.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 603)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
TITLE        Inferring nonneutral evolution from human-chimp-mouse orthologous
             gene trios
JOURNAL      Science 302 (5652), 1960-1963 (2003)
PUBMED       14671302
REFERENCE    2  (bases 1 to 603)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
TITLE        Direct Submission
JOURNAL      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
             Rockville, MD 20850, USA
COMMENT      This sequence was made by sequencing genomic exons and ordering
             them based on alignment.
FEATURES             Location/Qualifiers
     source          1..603
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1..>603
                     /locus_tag="HCM2274"
ORIGIN
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Query Match         28.9%;  Score 594;  DB 9;  Length 603;
Best Local Similarity   99.2%;  Pred. No. 2.7e-140;
Matches    597;  Conservative    0;  Mismatches    0;  Indels    5;  Gaps    0;

Qy   220  GGCAGGCTGTTTATTGTAATGTAATGGAATATTGTGATGGAGGGGATCTCATGAAAGGATCAAT  279
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  GGCAGGCTGTTTATTGTAATGTAATGGAATATTGTGATGGAGGGGATCTCATGAAAGGATCAAT  60

Qy   280  AGACAACGGGGTGTGTTATTTAGTGAAGATCAGATCCAGATCTCGGTTGGTTGTTTGTACAGATTTCT  339
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  AGACAACGGGGTGTGTTATTTAGTGAAGATCAGATCCAGATCTCGGTTGGTTGTTTGTACAGATTTCT  120

Qy   340  CTAGGACTAAAACATATTCATGACAGGAAGAATATTCACAGGACTTGGATTGGTCAAGAGTC  399
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CTAGGACTAAAACATATTCATGACAGGAAGAATATTCACAGGACTTGGATTGGTCAAGACGT  180

Qy   400  ATTTTTCTTAGCAAGAACCGAATGGTGGCAAAGCTTGGGACTTTGGGTATAGCAAGAGTC  459
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ATTTTTCTTAGCAAGAACGGAATGGTGGCAAAGCTTGGGACTTTGGTATAGCAAGAGTC  240

Qy   460  CTGAATAATTCCATGGAACTTGCTCGACAACTTGTATTGGAACACCTTACCTACCTGTCCCCA  519
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CTGAATAATTCCATGGAACTTGCTCGACAACTTGTATTGGAACACCTTACCTACCTGTCCCCA  300

Qy   520  GAGATCTGTCAGAATAAACCCTACAACATAAAACGGATATTTGTCTCTTGGCTGTGTC  579
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polyA_signal    2381..2386
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polyA_site      2407
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ORIGIN
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CWFVQISLGLKGHIHDRKILRDIKSQNIFLSKNGMVAKLGDFGTARTLNDSMELAQTC
AGTPYYLSPEICQNRPYNNKTDIWSLGCVLYELCTLKHPFESNNFHHLVLKICQGRVA
PISPHSRDLQSLIPLFRVSPQDRPSVTSLLKRPFLETIIARSLYPEVCSRRIQSHA
HMENMAIGPTACWRVSPWSAAYLQRKFEAQQYKLVVERQLGLRPSSVEPHPNEGEKLQ
SHWEETKFQELQYRKNKMKDQEYWKQLEBIRQQYHNDMKEIKKKMGRELKRVVKFEIS
LDKCISEEDTVQENEAVDKLNATLSPEDGYKFQHRCKEHEDYTDRAFEBLCGPEAE
GFFQDVIAAENRRQWDAGAPHTLLRIMAMADVTSTCPTMPDDGVIVMEGSVENGKQW
WLDVPGTTPCALAAEACSGSLSASKGETVMIKPQLPKEDQEKVEIATGIMVDDEQLEP
GSDEDDMQEGRGIKNSMPSSATSKIKASPGCMASCPNSVTPPPLQRKI"
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Query Match         29.0%;  Score 595.4;  DB 3;  Length 2407;
Best Local Similarity   81.0%;  Pred. No. 1.6e-140;
Matches    722;  Conservative    0;  Mismatches    156;  Indels    13;  Gaps    2;

Qy     1  ATGGATAAGTACGATGATGATTAAGGCCATGGCAAGCTGCCTTCGGGAAAGCATACTTA  60
               ||||  ||||| |||  |||||||||||||||||||||||||||||||||||||||
Db    92  ATGGATAAACTTTCACCTGATTAAGATCATTGGGAAGCATCATTGGGGAAGTGTACTTG  151

Qy    61  GCTAAAGGGAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG  120
               ||||| |||||| ||||| |||  || |||||||| |||||| || |||||  |||
Db   152  GCTAAAGATAAATCAGAAGCAGTCACTGTCACTGTCATAAAAGAAATCAGTTTGACAAG---  208

Qy   121  CCCATACAAGAAAAAAGAGAGCTTCAAAGAAGAAGTGATTCTTCTGAAAAGATGAAACAT  180
               ||||      ||||||||| ||||||| ||  ||||| || ||||||||| || |||||
Db   209  -------GAAAAAGAGGCCTCAAAGAACGAAGTGATTTCTCTGGCTAGGATGGAGCAT  259

Qy   181  CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAGAATGGCAGGCTTGTTTATTGTAATG  240
               ||||||||||||||||||| ||| |||||| |||||| ||||||||||||||||||||||
Db   260  CCCAATATCGTAACCTTCTTCAGCTCGTTTCAAGAGAACGGCAGGCTGTTTATTGTAATG  319

Qy   241  GAATATTGTGATGGAGGGGATCTCATGAAAAGAGATCAATAGACAACGGGGTGTGTTATTT  300
               ||||||||||||||||||||||||||  ||||||||| ||||||||||||||||||||||
Db   320  GAATACTGTGATGGAGGGGATCTCATGCAAGAGGCAGCCAGGCGCGGGAGTGATGTTC  379

Qy   301  AGTGAAGATCAGATCCTCCGGTTGGTTGTACAGATTATTCATGACAGGAAGAATATTCAT  360
               ||| ||||||| |||||||||||| ||||||||||||| ||||||||| |||||||||||
Db   380  AGCGAAGACCAGATCCGTGTTGGTTGTACAGATTTTCATGACAGGATTCAT  439

Qy   361  GACAGGAAGAATTACACAGGACAGGAACATTTTCTTAGCAAGAACGGA  420
               |||||||||  ||||||| ||||| |||||||||| ||||||||||||||
Db   440  GACAGGAAGAATTTTTACACAGGACATAAAATCTCAGAATAATTTCTCAGAAGAATGGA  499

Qy   421  ATGGTGGCAAAGCTTGGGACTTGGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480
               ||| |||||||||||||||||| |||||||||||||||| |||||||||||||||||||||
Db   500  ATGGTTGCCAAGCTCGGGGACTTCGGGGACTTTGGGGACATCGTGGGGAAGCTTGGGGACTTTGGGGACTTGGGGA  559

Qy   481  GCTCGACAACTTGTATTGGAACACCTTACCTGTCAGAATAAACCC  540
               ||||||||||||| ||| |||||||||||||| |||| ||||| |||
Db   560  GCTCAAACATGTGCTGGGGACACCTTACCTACTCTGTCCCCAGAGATCTGTCAGACAGGCCA  619

Qy   541  TACAACAATAAAACGGATATTTGGTCTCTTATATAGAGCTCTGCACACTT  600
               ||||||||||||||||||||||||||  ||||| ||  |||| ||||||||
Db   620  TACAACAATAAAACGGACATCTCGTGTCGTGTCGGCTGGTCGTGTGTGTTAGTAGAGCTCTGCACTC  679

Qy   601  AAACATCCTTTGAGGGGAACAACTTACACAGCAGCTGGTCGTTGTCAAGACACAT  660
               ||||||||||||||||| |||||| |||||||||||||||||||||||||||||||
Db   680  AAGCATCCTTTTGAGAGCAACAACAACTTGCCCACAATCTGGTTCCAAGAGATTTGTCAAGACGT  739

Qy   661  TTTGCCCAATATCTCCGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCCAGCTCTTT  720
               ||||  |||||| ||||  |||||| |||||| || |||||||||| ||||||||||||||
Db   740  GTTGCTCATACACCCCACTTCTCTCGTGACCTCAGTCGTTGATAACCTTGGTCGATATCCTCAGCTCTTTC  799

Qy   721  CAGTATCTCCGAGACCGACCATCCATAAATCCATATAAATTCATTGAAAAGGCCCTTTTAGAG  780
               ||||| ||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||
Db   800  AGAGTGTCTCCTCAGGACCGGCCATCCGGCCATCCGTTACGTCCGTTACCCTTTGAAAAGACCCTTTTTAGAA  859

Qy   781  AATCTTTATTCCCAAATATTTGACTCCTGAGGTC-ATTCGAGGAAGAATTCAGTCACATGCT  839
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Db  301  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  204  TTCATTTCAAGAGAATGGCAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGGATCT  263
Qy  580  TTATATGAGCTCTGCACACTTAAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTT  639    Qy  51   TTTTCTTACAGAGAATGGCAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGGATCT  110
Db  361  TTATATGAGCTCTGCACACTTAAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTT  420    Db  264  CATGAAAAGGATCAATAGACAACGGGGTGTGTTATTTAGTGAAGATCAGATCCTCGGTTG  323
Qy  640  CTGAAGAGTTGTCAAGCACATTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCAT  699   Db  111  CATGAAAAGGATCAATAGACAACGGGGTGTGTTATTTAGTGAAGATCAGATCCTCGGTTG  170
Db  421  CTGAAGAGTTGTCAAGCACATTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCAT  480   Qy  324  GTTTGTACAGATTTCTCTAGGACTAAAACATATTCATGCACAGAAGAATATTACCACAGGGA  383
Qy  700  TCCTTGATATCTCAGCTCTTTCAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATT  759   Db  171  GTTTGTACAGATTTCTCTAGGACTAAAACATATTCATGCACAGAAGAATATTACCACAGGGA  230
Db  481  TCCTTGATATCTCAGCTCTTTCAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATT  540   Qy  384  CATAAAAGCTCAGAACATTTTCTTACAGAAGACGGAATGGTGGCAAAGCTTGGGGACTT  443
Qy  760  TTGAAAAGGCCCTTTTTAGAGAATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAG  819   Db  231  CATAAAAGCTCAGTAACAGCTCAGAGAGAAGACTAAGCACAGACTGATCTTTTCTTGAA  290
Db  541  TTGAAAAGGGCCCTTTTTAGAGAATCTTATTCCCAAATATTTGACTCCTGAGGTAAGTTTT  600   Qy  444  TGGTATAGCAAGAGTCCTGAATAATTCCATGAAGACTTGCTCGAACTTGTATTGGAACACC  503
Qy  820  GA   821   Db  291  GTACCTCAAACACACATGACATTTTCTCCATTATAGAACATTTTCTTAGCAAGAACGA  350
Db  601  GA   602   Qy  504  TTACTACCTGTCCCAGAGATCTGTGCAGAATAAAACCCTACAACAATAAAACGGATATTTG  563
                                                                        Db  351  ATGGTGGCAAAGCTTGGGGACTT---TGGTATAGCAAGAGTCCTGAATAAGAATATTTG  406
                                                                        Qy  564  GTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTTAAACATCCTTTTGAGGGTAACAA  623
                                                                        Db  407  GTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTTAAACATCCTTTTGAGGGTAACAA  466
                                                                        Qy  624  CTTACAGCAGCTGGTTCTCGAAGATTTGTCAAGCACACATTTGCCCCAATATCTCCGGGGTT  683
                                                                        Db  467  CTTACAGCAGCTGGTTCTCGAAGATTTGTCAAGCACACATTTTGCCCCAATATCTCCGGGGTT  526
                                                                        Qy  684  TTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTTCAAGTATCTC-CTCGAGACCGAC  742
                                                                        Db  527  TTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTTCAAGTATCTCTCTCGAGACCGAC  586
                                                                        Qy  743  CATCCATAAATTCCATTTGAAAAGGCCCTTTTTGAGAGAATCTTATTCCCAAATATTGA  802
                                                                        Db  587  CATCCATAAATTCCATTTGAAAAGGGCCCTTTTTGAGAGAATCTTATTCCCAAATATTGA  646
                                                                        Qy  803  CTCCTGAGGTCATTCAGGAAGGTCCATTCAGTCACATGCTTATATGCAGAGCAGCAGGCGCCAG  862
                                                                        Db  647  CTCCTGAGGTCATTCAGGAAGGTCCATTCAGTCACATGCTTATATGCAGAGCAGCAGGAGCGCCAG  706
                                                                        Qy  863  CTTCTCGACATGCTGGGAAGGTGGTCCAGAAGTGTAA-ATACAAAAAGTGAGATTCCAG  921
                                                                        Db  707  CTTCTCGACATGCTGGGAAGGTGGTCCAGAAGTGTAAACATACAAAAAGTGAGATTCCAG  766
                                                                        Qy  922  GGAAAGTGCCCACCAAGATCAAGGATATCTGTGCCAATTAAAAGGAATGCTATATTGCAT  981
                                                                        Db  767  GGAAAGTGCCCACCAAGATCAAGGATATCTGTGCCAATTAAAAGGAATGCTATATTGCAT  826
                                                                        Qy  982  AGAAATGAATGGAGA-CMCCAGCTGTGGAGCCCAGAAGGCCAGATCTA  1027
                                                                        Db  827  AGAAATGAATGGAGA-CMCCAGCTGTGGAGCCCAGAAGGCCAGATCTATA  871
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RESULT 7
BX417448
LOCUS   BX417448   872 bp   mRNA   linear   EST 01-MAY-2004
DEFINITION   BX417448 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YJ07
             5-PRIME, mRNA sequence.
ACCESSION   BX417448
VERSION   BX417448.2 GI:46926799
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 872)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   On May 13, 2003 this sequence version replaced gi:30642067.
             Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France
             Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
             1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
             end enriched, double-strand cDNA was digested with Not I and cloned
             into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
             was not normalized. Library was constructed by Life Technologies, a
             division of Invitrogen.
             This sequence belongs to sequence cluster 6942.r.
             There is a virtual cDNA representing this cluster. For more
             information about this cluster and the virtual cDNA, see
             http://www.genoscope.cns.fr/cdna?s=CS0DE009CE04QP1&c=6942.r.
FEATURES   Location/Qualifiers
     source   1..872
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                     /clone="CS0DE009YJ07"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

Query Match   28.1%; Score 576.4; DB 5; Length 872;
Best Local Similarity 84.3%; Pred. No. 9.2e-136;
Matches 696; Conservative 1; Mismatches 122; Indels 7; Gaps 4;

RESULT 8
CD700193
LOCUS   CD700193   670 bp   mRNA   linear   EST 25-JUN-2003
DEFINITION   EST16717 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD700193
VERSION   CD700193.1 GI:32230189
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 670)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
             Zeng,Y.-X.
  TITLE   Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)

COMMENT   Contact: YiXin Zeng
               Cancer Center
               Sun Yat-sen University
               651 DongFeng Road East, GuangZhou 510060, China
               Tel: 86-1380-9770-743
               Fax: 86-20-8775-4506
               Email: yxxeng@gzsums.edu.cn.

FEATURES   Location/Qualifiers
   source   1..670
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /tissue_type="normal nasopharynx"
               /clone_lib="human nasopharynx"
               /note="ESTs generated from a normal nasopharynx cDNA
               library from southern Chinese"

ORIGIN

Query Match   26.2%;   Score 536.8;   DB 6;   Length 670;
Best Local Similarity 99.6%;   Pred. No. 1.1e-125;
Matches 538; Conservative   0; Mismatches   0; Indels   0;   Gaps   0;

Qy   1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCGAAGGTGCCTTCGGGAAAGCATACTTA   60
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Db   116 ATGGATAAGTACGATGTGATTAAGGCCATCGGCGAAGGTGCCTTCGGGAAAGCATACTTA 175

Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   176 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 235

Qy   121 CCCATACAAGAAAAGAAGCTTCAAAGAAAGTGATTCTTCTGGAAAGATGAAACAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   236 CCCATACAAGAAAAGAAGCTTCAAAGAAAGTGATTCTTCTGGAAAGATGAAACAT 295

Qy   181 CCCAACATTGTAGCCTTCTCAATTCATTCAAGAGAGATGGCAGGCTGTTATTGTAATG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   296 CCCAACATTGTAGCCTTCTCAATTCATTCAAGAGAGATGGCAGGCTGTTATTGTAATG 355

Qy   241 GAATATTGTGATGCGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATTT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   356 GAATATTGTGATGCGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATTT 415

Qy   301 AGTGAAGATCAGATCCCTCGGTTGGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   416 AGTGAAGATCAGATCCCTCGGTTGGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 475

Qy   361 GACAGGAAGATATTACACAGGGACATTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   476 GACAGGAAGATATTACACAGGGACATTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACGGA 535

Qy   421 ATGGTGGCAAAGCTTGGGACTTGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   536 ATGGTGGCAAAGCTTGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 595

Qy   481 GCTCGAACTTGTATTCGGAACACCTTACACCTTACACTGTCCCCAGAGATCGTGTCAGAATAAACCC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   596 GCTCGAACTTGTATTCGGAACACCTTACACCTTACACTGTCCCCAGAGATCGTGTCAGAATAAACCC 655

RESULT 9
BQ917635
LOCUS   BQ917635   AGENCOURT 8888753 NIH_MGC_129   928 bp   mRNA   linear   EST 20-AUG-2002
DEFINITION   5', mRNA sequence.   AGENCOURT 8888753 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6311513
ACCESSION   BQ917635
VERSION   BQ917635.1   GI:22332333
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 928)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.

TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Susan L. Sullivan, Ph.D.
             cDNA Library Preparation: ResGen, Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM13735 row: i   column: 18
             High quality sequence stop: 734.

FEATURES   Location/Qualifiers
   source   1..928
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             /mol_type="mRNA"
             /db_xref="taxon:10090"
             /clone="IMAGE:6311513"
             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH_MGC_129"
             /note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;
             Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
             Primer: Oligo dT. Average insert size 2.2 kb. Constructed
             by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
             Library."

ORIGIN

Query Match   25.1%;   Score 514.8;   DB 5;   Length 928;
Best Local Similarity 81.1%;   Pred. No. 5e-120;
Matches 640; Conservative   0; Mismatches 133; Indels 16; Gaps 3;

Qy   1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCGAAGGTGCCTTCGGGAAAGCATACTTA   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   93 ATGGATAACTTCACCTGATTAAGATCATTGGGGAAGGAGGCACCTTTGGGAAGGTGTACTTG 152

Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 120
          |||||| |||||| |||||||||||||||||||||||||||||| ||||| |||||
Db   153 GCTAAAGATAAATCAGAAGCAGTCACTGTGTCATAAAAGAAATCAGTTTGAAAAG--- 209

Qy   121 CCCATACAAGAAAAGAAGCTTCAAAGAAAGAAGTGATTCTTCTGGAAAGATGAAACAT 180
          ||||||| ||||||||||||||||| |||||| ||||||| ||||||||||||
Db   210 ------GAAAAAGAGAGGCCTCAAAGAACGAAGTGATTCTTCTGGCCTAGGATGATGGAGCAT 260

Qy   181 CCCAACATTGTAGCCTTCTCAATTCATTCAAGAGAGATGGCAGGCTGTTATTGTAATG 240
          |||||||||||| |||||||||| |||||||||||||||||| ||||||||| |||||
Db   261 CCCAATATCGTAACCTTCTCAGCTCGTTCAAGAAGGATCAATAGACAACGGGGTGTGTTATTT 320

Qy   241 GAATATTGTGATGCGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATTT 300
          |||||||||| ||| ||||||||| ||||||| |||||||||||||||||||||||||||||
Db   321 GAATACTGTGATGGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGGAGTGATGTTC 380

Qy   301 AGTGAAGATCAGATCCCTCGGTTGGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 AGCGGAAGACCAGATCCCTCGGTTGGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 440

Qy   361 GACAGGAAGATATTACACAGGGACATTTGGTATAGCAAGCAATAAATTCCAGAATCCAGTTCT 420
          ||||||||||||||||||||||| |||||||||||||||| ||||||| ||||||||
Db   441 GACAGGAAGAGATTTTACACAGGGACATTTGGAATATAGTAGATCTTATATGACAACGGA 500

Qy   421 ATGGTGGCAAAGCTTGGGACTTTGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
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Db   501 ATGGTTGCCAAGCTCGGGGACTTTGGAACAGCAGCAGCAAGAACTGAATGACTCCATGGAACTT 560

Qy   481 GCTCGAACTTGTATTCGGAACACCTTACACCTTACACTGTCCCCAGAGATCGTGTCAGAATAAACCC 540
          ||||||||||| ||||||| ||||||||||||||||||||||||||||||||||||
Db   561 GCTCAAACATGTGCTGGACACCTTACTACTCCCCAGAGATCGTCAGAACAGGCCA 620

Qy   541 TACAACAATAAAACCGATATTGGTCTCTTGGTGTCCTTATATGAGCTCTGCACACTT 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   621 TACAACAATAAAACCGACATCGGTCTCTTGGCTGTCTTATATGAGCTCTGCACACTC 680

Qy   601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACAT 660

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Db  268 CCCATACAAGAGAAAAGAAGCTTCAAAGAAGAAGAGTGATTCTTCTGGAAAGATGAAACAT 327
            ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Qy  181 CCCACACATTGTAGCCTTCTTCAATCATTCAAGAGAATGGCAGGCTGTTTATTGTAATG 240
            ||||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||
Db  328 CCCACACATTGTAGCCTTCTTCAATCATTCAAGAGAATGGCAGGCTGTTTATTGTAATG 387

Qy  241 GAATATTGTGATGGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATTT 300
            |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  388 GAATATTGTGATGGAGGGGATCTCATAGACAATCAATAGACAACAACGGGGTGTGTTATTT 447

Qy  301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTCTCTAGGACTAAAACATATTCAT 360
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Db  448 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCAGGACTAAAACATATTCAT 507

Qy  361 GACAGGAAGATATTACACAGGGACATACAGGGACATATTTCTTAGCAAGAACCGA 420
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Db  508 GACAGGAAGATATTACACAGGGACATACAGGGACATATTTTCTTAGTCAGAACGGA 567

Qy  421 ATGGTGCGAAAGCTTGGGGACTTTGGTATAGCAAGAGT-CCTGAATAATTCAT-GGAAC 478
            |||||||||||||||||||||||||||||||||||||  |||||||||||||| |||||
Db  568 ATGGTGCGAAAGCTTGGGGACTTTGGTATAGCAAGAATCCCTGAATAATTCCATGGGAAC 627

Qy  479 TTGCTCGAACTTGTATTGG--AACACCTTACTACCTGTCCCC---AGAGATCTGTCAGA 532
            |||||||||||||||||||  |||||||||||| |||||||||    ||||||||||||
Db  628 TTGCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGAGATCTGTCAGAA 687

Qy  533 ATAAACCTACAACAATAAAACGGATATTT 562
            |||||||||||||||||||||||||||||
Db  688 TAAAACCCTACAACAATTAAAACGGGATAT 717
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RESULT 11
AY405589
LOCUS   AY405589   603 bp   DNA   linear   GSS 12-DEC-2003
DEFINITION   Pan troglodytes HCM2274 gene, VIRTUAL TRANSCRIPT, partial sequence,
              genomic survey sequence.
ACCESSION   AY405589
VERSION   AY405589.1 GI:39761563
KEYWORDS   GSS.
SOURCE   Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1 (bases 1 to 603)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
              gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 603)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
              Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
              them based on alignment.
FEATURES   Location/Qualifiers
     source   1..603
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene   <1..>603
                     /locus_tag="HCM2274"
ORIGIN
Query Match   22.7%;   Score 464.8; DB 9; Length 603;
Best Local Similarity 77.9%; Pred. No. 2.7e-107;

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Db  681 AAGCATCCTTTGAGAGCAACAACTTCACCATCTGGTTCTGAAGATTGTCAAGGACGT 740
            ||||||||||||||||||||||||||||||| |||||||  ||   ||||||||||
Qy  661 TTGCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCC--TTGATATCTCAGCTCT 718
            ||||||||||||||||| ||||||||||  ||||||  |   |||||||||||||||||
Db  741 GTTGTCCCATATCACCCCCACTTCTCTCGTGACCTACAGTNCCTGATACCCTCAGCTCT 800

Qy  719 TTCAAGTATCTCCTCGAGACC--GACCATCCATAAATTCCATTTGAAAAGGCCCTTTT 776
            ||| || || |||||||  |   |||||||||||| ||||||||||||||||||||||||
Db  801 TCAGAGTGTCTCCTCCCAGGACCCGGCCATCCGGCATCCCGTTACGTCCCCTTTTGAAAAAGACCCCTTTT 860

Qy  777 AGAGAATCT 785
            ||||| ||
Db  861 TTAGAAACT 869
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RESULT 10
CD243608
LOCUS   CD243608   856 bp   mRNA   linear   EST 22-MAY-2003
DEFINITION   AGENCOURT 14121106 NIH_MGC_180 Homo sapiens cDNA clone
              IMAGE:30383658 5', mRNA sequence.
ACCESSION   CD243608
VERSION   CD243608.1 GI:31004072
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 856)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Dr. Michael Brownstein
              cDNA Library Preparation: Invitrogen Corp
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: NDAM447 row: n column: 19
              High quality sequence stop: 545.
FEATURES   Location/Qualifiers
     source   1..856
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30383658"
                     /clone_lib="NIH_MGC_180"
                     /lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
                     /note="Organ: Testis; Vector: pCMV-SPORT6.1; Site_1: NotI;
                     Site_2: EcoRV (destroyed); Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.68 kb. Library was
                     constructed by (Invitrogen). Note: this is a NIH_MGC
                     Library."
ORIGIN
Query Match   23.1%;   Score 474; DB 6; Length 856;
Best Local Similarity 94.2%; Pred. No. 1.3e-109;
Matches 537; Conservative 0; Mismatches 25; Indels 8; Gaps 4;

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Qy    1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  148 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTA 207

Qy   61 GCTAAAGGGAAAATCAGATAGCAAGCAAGCTGTCATAAAAGAGATCAATTTTGAAAAGATG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  208 GCTAAAGGGAAAATCAGATAGCAAGCAAGCTGTCATAAAAGAGATCAATTTTGAAAAGATG 267

Qy  121 CCCATACAAGAGAAAAGAAGCTTCAAAGAAGAAGAGTGATTCTTCTGGAAAGATGAAACAT 180
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TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
             Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
             them based on alignment.
FEATURES   Location/Qualifiers
    source   1..603
             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /db_xref="taxon:10090"
    gene   <1..>603
             /locus_tag="HCM2274"
ORIGIN

Query Match   22.2%;   Score 455.4; DB 9; Length 603;
Best Local Similarity   84.9%; Pred. No. 6.7e-105;
Matches 510; Conservative   0; Mismatches   91; Indels   0; Gaps   0;

Qy   220 GGCAGGCTGTTGTTATTGTAATGGAATATTGTGATGGAGGGGATCTCATGAAAAGGATCAAT 279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGCAGGCTGTGTTATTGTAATGGAATACTGTGATGGAGGGGATCCATGCAGAGGATCCAG   60

Qy   280 AGACAACGGGTGTGTTATTTAGTGAAGATCAGATCCTCGGTTGGTTTGTTACAGATTTCT 339
           ||||||||||||||||||||||| |||||||| ||| || | ||||||||| ||||||||
Db   61 AGGCAGCGGGGAGTGATGTTCAGCGAAGACCAGATCCTCGTGTTGGTTTGTTACAGATTTCT 120

Qy   340 CTAGGACTAAAACATATTCATGACACAGGAGATATTACACAGGGACATAAAAGCTCAGAAC 399
           |||||||||||||||||||||||||||||||||||| ||||| |||||||||||||||||
Db   121 CTAGGACTGAAGCATATTCATGACACAGGAGAAGAAGATTTTACACAGGGACATAAAATCTCAGAAT 180

Qy   400 ATTTTTCTTAGCAAGAACGGATGGTGCAAAGCTTGGGACTTTGGGTATAGCAAGAGTC 459
           |||||||||||||||||||||||||||| |||||||| |||||||||||||||||||||
Db   181 ATTTTTCTTAGCAAGAACGGATGGTGCAAAGCTTGGCAAGCTCGGGGACTTTGGGTATAGCAAGAACA 240

Qy   460 CTGAATAATTCCATGGAACTTGCTCGAACTGTATTGGAACACCTTACTACCTGTCCCA 519
           |||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   241 CTGAATAATTCCATGGAACTGGCTCAAACATGTCTCAAACATGTCTGGGACACCTTACTACCTGTCCCA 300

Qy   520 GAGATCTGTCAGAATAAACATCCTTTGGTCTCTTGGCTGTGTC 579
           |||||||||||||||||||||||||||||||||||||||||||
Db   301 GAGATCTGTCAGAACGAGCGCCATCACAACAAACGACATCTGGTCTCTTGGCTGTGTC 360

Qy   580 TTATATGAGCTCTGCACACTTAAACATCCTTTGAGGTAACAACTTACAGCAGCTGGTT 639
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TTATATGAGCTCTGCACACTTCAAGCATCCTTTGAGAGCAACAACACTTCCACCATCTGTT 420

Qy   640 CTGAAGATTTGTCAAGCACATTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCAT 699
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTGAAGATTTGTNNNGCACATTTGCCCCAATATCTCCGAGACCGACCATCCACCTTCCATT 480

Qy   700 TCCTTGATATCTCAGCTCTTCAGGGTGTGTTCCTCAGAGTAATCTTATTCCCAAATATTCCATT 759
           |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCTTGATATCTCAGCTCTTCNNGGGGACCGCCATCCATCCATAAATTCCATT 540

Qy   760 TTGAAAAGGCCCTTTTAGAGAATCTTATTCCCAAATATTTGACTCGTCATTCATTCAG 819
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TTGAAAAGACCCTTTTTAGAAACTCTCATTGCCGATCCTTGTATCCTTGAGGTAGGTCTG 600

Qy   820 GA 821
           | |
Db   601 GA 602

RESULT 12
AY405590
LOCUS   AY405590   603 bp   DNA   linear   GSS 12-DEC-2003
DEFINITION   Mus musculus HCM2274 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION   AY405590
VERSION   AY405590.1 GI:39761564
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 603)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
             gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 603)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.

Matches 469; Conservative   0; Mismatches 133; Indels   0; Gaps   0;

Qy   220 GGCAGGCTGTTGTTATTGTAATGGAATATTGTGATGGAGGGGATCTCATGAAAAGGATCAAT 279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGCAGGCTGTGTTATTGTAATGGAATACTGTGATGGAGGGGATCCATGCAGAGGATCCAG   60

Qy   280 AGACAACGGGTGTGTTATTTAGTGAAGATCAGATCCTCGGTTGGTTTGTTACAGATTTCT 339
           ||||||||||||||| ||||||||| || ||||| |||| || || |||||||||||||||
Db   61 AGACAACGGGGTGTGTTATTTAGTGAAGATCANNNNCTCGGTTGGTTTGTTACACNGATTTCT 120

Qy   340 CTAGGACTAAAACATATTCATGACACAGGAGATATTACACAGGGACATAAAAGCTCAGAAC 399
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CTNGGACTAAAACATATTCATGACACAGGAGATATTACACAGGGACATAAAAGCTCAGAAC 180

Qy   400 ATTTTTCTTAGCAAGAACGGATGGTGCAAAGCTTGGGACTTTGGGTATAGCAAGAGTC 459
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATTTTTCTTAGCAAGAACGGATGGTGCAAAGCTTGGGACTTTGGGTATAGCAAGAGTC 240

Qy   460 CTGAATAATTCCATGGAACTTGCTCGAACACCTGTTACTACCTGTCCCCA 519
           ||||||||| ||||||
Db   241 CTGAATAATANNNNNNNNNNNNNNNNNNNNN 300

Qy   520 GAGATCTGTCAGAATAAACATCCTTTGGTCTCTTGGCTGTGTC 579

Db   301 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 360

Qy   580 TTATATGAGCTCTGCACACTTAAACATCCTTTGAGGGTTT 639
           |||||||||||||||||||||||||||
Db   361 TTATATGAGCTCTGCACACTTAAACATCCTNNNNNNNNNNNNNNNNNNNGTT 420

Qy   640 CTGAAGATTTGTCAAGCACATTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCAT 699
           |||||||||||||||||||||||||||||||||||||||||||
Db   421 CTGAAGATTTGTNNNGCACATTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTACAT 480

Qy   700 TCCTTGATATCTCAGCTCTTCAGAGTGATCTCGAGACCGACCATCCATAAATTCCATT 759
           |||||||||||||||||||| || ||||||||||||||||||||||||||||||||||
Db   481 TCCTTGATATCTCAGCTCTTCNNGATCTCCGAGACCGACCATCCATAAATTCCATT 540

Qy   760 TTGAAAAGGCCCTTTTTAGAGAATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAG 819
           |||||||||||||||||| |||||||||||
Db   541 TTGAAAAGGCCCTTTTTAGAGAATCTTATTCCCAAATATTTGACTCCTGAGGTAAGTTTT 600

Qy   820 GA 821
           | |
Db   601 GA 602

RESULT 13
BB666328
LOCUS   BB666328   659 bp   mRNA   linear   EST 26-OCT-2001
DEFINITION   BB666328 RIKEN full-length enriched, 2 days pregnant adult female
             ovary Mus musculus cDNA clone E330012F19 5', mRNA sequence.
ACCESSION   BB666328
VERSION   BB666328.1 GI:16499961
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus

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Query Match            22.0%;
Best Local Similarity  84.8%;    Score 452.4;  DB 2;   Length 659;
Matches  507;  Conservative  0;  Mismatches  91;  Indels  0;  Gaps  0;
                                 Pred. No. 4e-104;

Qy     213 AGAGAATGGCAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGGGATCCATGAAAAG 272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      53 AGAGAACGGCAGGCTGTTTATTGTAATGGAATACTGTGATGGAGGGGGATCCATGCAGAG 112

Qy     273 GATCAATAGACACACGGGGTGTGTTATTAGTGAAGATCAGAATCCTCGGTTGGTTTGTACA 332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     113 GATCCAGAGGCAGCGGGGAGTGATGTTCAGCGAAGACCAGATCCTGTGTTGGTTTGTACA 172

Qy     333 GATTTCTCAGGACTAAAACATATTCATGACAGGAAGATATTACACAGGGACATAAAAGC 392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     173 GATTTCTCAGGACTGAAGCATATTCATGACAGGAAGAATTTTACACAGGGACATAAAATC 232

Qy     393 TCAGAACATTTTTCTTAGCAAGAACGAATGGTGGCAAAGCTTGGGAGCTTTGGTATAGC 452
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     233 TCAGAATATTTTTCTTAGCAAGAATGGAATGGTTGCCAAGCTCGGGGACTTTGGAACAGC 292

Qy     453 AAGAGTCCTGAAATAATTCCATGGAACTTGCTGCAGAACTTGTATTGGAACACCTTACTACCT 512
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     293 AAGAACACTGAATGACTTCCATGAACTTGCTCAAACATGTGGCTGGGCACCTTACTACCT 352

Qy     513 GTCCCCAGAGATCTGTCAGAATAAACCCTACAACAATAAACCGATATTTGGTCTCTTGG 572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     353 GTCCCCAGAGATCTGTCAGACACGAGGCCATAACACCAATAAAAACGGACATCTGGTCTCTTGG 412

Qy     573 CTGTGTCTTATATGAGTCTGCACACTTAAAACATCCTTTGAGGGTAACAACTTACAGCA 632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     413 CTGTGTCTTATATGAGTCTGCACACTCAAGCATCCTTTGAGGCAACAACTTCCACCA 472

Qy     633 GCTGGTTCTGAAGATTGTCAAGCACATTTGCCCCAATATCTCCGGGGTTTCTCGTGA 692
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     473 TCTGGTTCTGAAGATTTGTCAAGGACGTGTTCCTCCCATATCACCCCACTTCTCTCGTGA 532

Qy     693 GCTCCATTCCTGATATCTCAGCTCTTCAAGTATCCTCGAGACCGGACCATCCATAAA 752
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     533 CCTACAGTCTTGTATACCTCAGCTCTTCAGTGTCTCTCAGGACGGCACCCGGTAC 592

Qy     753 TTCCATTTTGAAAAGGCCCTTTTGAAGAATCCTATTCCCAAATATTTGACTCCTGAG 810
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     593 GTCCCTTTTGAAAAGACCCTTTTAGAAACTCTCCATTGCCCGATCCTTTGTATCCTGAG 650
```

```
RESULT 14
BX328262
LOCUS       BX328262                          678 bp    mRNA     linear    EST 08-APR-2004
DEFINITION  BX328262 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL005YK18 5-PRIME, mRNA sequence.
ACCESSION   BX328262
VERSION     BX328262.2  GI:46281652
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 2, 2003 this sequence version replaced gi:30344693.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            6942.r,
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REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  AUTHORS   1 (bases 1 to 659)
             Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
             Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,N., Kawai,J.,
             Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
             Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
             Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
             Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
             Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
  TITLE   RIKEN Mouse ESTs (Arakawa,T., et al 2001)
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Yoshihide Hayashizaki
             Laboratory for Genome Exploration Research Group, RIKEN Genomic
             Sciences Center(GSC), Yokohama Institute
             The Institute of Physical and Chemical Research (RIKEN)
             1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
             Tel: 81-45-503-9222
             Fax: 81-45-503-9216
             Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
             Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new
             genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
             Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
             Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
             and Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer. Genome Res.
             10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
             Sugahara,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
             encyclopedia: real-time sequence clustering for construction of a
             nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
             Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
             Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
             Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
             further details.

```
FEATURES             Location/Qualifiers
     source          1..659
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="E330012F19"
                     /sex="female"
                     /tissue_type="ovary"
                     /dev_stage="2 days pregnant adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, 2 days pregnant
                     adult female ovary"
                     /note="Site 1: SalI; Site 2: BamHI; cDNA library was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'-
                     GAGAGAGAGATTCTCGAGTTAATTAATTAATCCCCCCCCCCCC 3']. cDNA
                     was cleaved with BamHI and XhoI. Vector: a modified
                     pBluescript KS(+) after bulk excision from Lambda FLC I."
ORIGIN
```

and it belongs to a clone representative of this cluster. For more information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?s=CS0BAG054ZE01_CS05093_1&c=6942.r

FEATURES   Location/Qualifiers
source   1..678
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="CS0DL005YK18"
             /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
             /cell_line="RAMOS CELL LINE"
             /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
             /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match   21.8%; Score 447.8; DB 5; Length 678;
Best Local Similarity 99.6%; Pred. No. 6e-103;
Matches 449; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy   759 TTTGAAAAGGCCCTTTTTAGAGAATCTTATTCCCAAATATTGACTCCTGAGGTCATTCA 818
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   45 TTTGAAAAGGCCCTTTTTAGAGAATCTTATTCCCAAATATTGACTCCTGAGGTCATTCA 104

Qy   819 GGAAGAATTCAGTCACATGCTATATGCAGAGCAGGAGCGCCAGCTTCTGACATGCTGG 878
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   105 GGAAGAATTCAGTCACATGCTATATGCAGAGCAGGAGCGCCAGCTTCTGACATGCTGG 164

Qy   879 GAAGGTGGTCCAGAAGTGTAAAATACAAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAG 938
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Qy   939 ATCAAGGATATCTGTCGTGCCAATTAAAAGGAATGCTATATTGCATAGAAATGAATGAGACC 998
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Qy   999 ACCAGCTGGAGCCCAGAAGGCCAGATCTATAAAAAATGATAGAAAAGACCCAAAATTGCTGC 1058
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Qy   1059 TGTCTGTGGACATTATGATTATTATTATGCTCAACTGATATGCTGAGGAGGAGAGCCCA 1118
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Qy   1179 AACGAGGCATGGTCCATCCCCAAGTCAATGG 1209
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RESULT 15
BB623078
LOCUS   BB623078   639 bp   mRNA   linear   EST 26-OCT-2001
DEFINITION BB623078 RIKEN full-length enriched, 10 days neonate cerebellum Mus musculus cDNA clone 6530411J22 5', mRNA sequence.
ACCESSION   BB623078
VERSION   BB623078.1 GI:16461881
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 639)
AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,

TITLE   Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Saaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
            RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL   Unpublished (2001)
COMMENT   Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp. URL:http://genome.gsc.riken.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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            Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
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            Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
            Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
            e mouse tissues.

FEATURES   Location/Qualifiers
source   1..639
             /organism="Mus musculus"
             /mol_type="mRNA"
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             /db_xref="taxon:10090"
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             /lab_host="DH10B"
             /clone_lib="RIKEN full-length enriched, 10 days neonate cerebellum"
             /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 100.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAAATTAATCCCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC II. Cloning sites, 5' end: SalI; 3' end: BamHI"

ORIGIN

Query Match   19.0%; Score 390; DB 2; Length 639;

Best Local Similarity 82.7%;   Pred. No. 3.4e-88;
Matches 463;   Conservative   0;   Mismatches   85;   Indels   12;   Gaps   1;

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Qy  181 CCCAACATTGTAGCCTTCTTCAATTCATTTCAGAGAGAATGGCAGGCTGTGTTATTGTAATG 240
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Qy  241 GAATATTGTGATGGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATTT 300
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Qy  361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
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Qy  421 ATGGTGGCAAAGCTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
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Db  620 TACAACAATAAAACGGACAT 639
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Search completed: October 10, 2004, 11:30:09
Job time : 9621 secs

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                GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   October  9, 2004, 22:26:00 ; Search time 1426 Seconds
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Title:          US-09-940-921B-1
Perfect score:  2052
Sequence:  1 atggataagtacgatgtgat.........cagtgctcatcctgatgtga 2052

Scoring table:  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:       4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters:   8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      11: geneseqn2003ds:*
      12: geneseqn2004s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2052	100.0	2052	6	ABK12424	Abk12424 cDNA enco
2	2052	100.0	2240	6	ABK12426	Abk12426 Novel hum
3	1976.4	96.3	2816	12	ADJ96571	Adj96571 Human Nim
4	1868	91.0	1965	6	ABK12425	Abk12425 cDNA enco
5	1654	80.6	2370	8	ABS57149	Abs57149 Human cDN
6	1469.6	71.6	1947	4	AAS06745	Aas06745 Polynucle
7	1359.8	66.3	1896	8	ABZ59716	Abz59716 Human NEK
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24	368	17.9	5532	12	ADB48335	Adb48335 Novel hum
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ALIGNMENTS

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RESULT 1
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ID   ABK12424 standard; cDNA; 2052 BP.
XX
AC   ABK12424;
XX
DT   18-JUN-2002  (first entry)
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DE   cDNA encoding novel human kinase protein #1.
XX
KW   Novel human protein; NHP; serine-threonine kinase; brain;
KW   calcium/calmodulin-dependent kinase; myosin light chain kinase;
KW   biological disorder; spleen; placenta; chromosome 6; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
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FT                  /product= "Human kinase protein #1"
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XX
PD   07-MAR-2002.
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PF   28-AUG-2001; 2001WO-US026776.
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PR   31-AUG-2000; 2000US-0229280P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Friddle CJ, Hilbun E, Nepomnichy B, Hu Y;
XX
DR   WPI; 2002-292200/33.
DR   P-PSDB; AAU77928.
XX
PT   Novel polynucleotide encoding novel human protein sharing structural
PT   similarity with animal kinases e.g. serine-threonine, calcium/calmodulin-
PT   dependent, and myosin light chain kinases, useful as probes and primers.
XX
PS   Claim 1; Page 37-38; 46pp; English.
XX
CC   The present invention relates to the isolation of novel human proteins
CC   (NHPs) and the polynucleotide sequences encoding them. The NHPs of the
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CC   invention are kinase proteins and share structural similarity to serine-
CC   threonine, calcium/calmodulin-dependent, and myosin light chain kinases.
CC   The sequences of the invention are useful for treating biological
CC   disorders. The polynucleotide sequences encoding the kinase proteins can
CC   be used as primers and probes. The sequences are also useful for
CC   identifying mutations associated with a particular disease and also in a
CC   prognostic or diagnostic assay. The present sequence encodes human
CC   protein kinase #1 which is expressed in a broad range of human tissues
CC   such as brain, spleen, and placenta. The gene encoding protein kinase #1
CC   is located on chromosome 6
XX
SQ   Sequence 2052 BP; 698 A; 388 C; 482 G; 484 T; 0 U; 0 Other;

Query Match           100.0%;   Score 2052;   DB 6;   Length 2052;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 2052;   Mismatches 0;   Conservative 0;   Indels 0;   Gaps 0;
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Qy    421 ATGGTGGCAAAGCTTGGGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT  840
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Qy    841 ATATGCAGAGCAGGAGCGCCAGCTTCTCGACATGCTGTGTCTGTGGGAAGGTGGTCCAGAAGTGTAAA  900
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Qy    901 ATACAAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATCAGGAGATATCTGTGCCAATT  960
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Qy   1501 AAAACCTATTTGGTGAAGAAGAGTAACCTGCCTGTCCTGCTTCAGAACAAATGAGGGCTTCAGAACAAAGGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AAAACCTATTTGGTGAAGAAGAGTAACCTGCCTGTCCTGCTTCAGAACAAATGAGGGCTTCAGAACAAAGGAA 1560

Qy   1561 GCACCTGTGCAGGACATTGAAAAGACTTGAAACAAATGAATGTGTAAAGGAGCAT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GCACCTGTGCAGGACATTGAAAAGACTTGAAACAAATGAATGTGTAAAGGAGCAT 1620

Qy   1621 AGTAAAAATCCAGAACAGAACAGAAATATAAAGCTAAGAGGGGTAAAATTGAAATTTAATTTA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AGTAAAAATCCAGAACAGAACAGAAATATAAAGCTAAGAGGGGTAAAATTGAAATTTAATTTA 1680

Qy   1681 GACAAATGTATTTCTGATGAAAAACATCCTCCAAGAGGAGAGGCAATGGATATACCAAAT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GACAAATGTATTTCTGATGAAAAACATCCTCCAAGAGGAGAGGCAATGGATATACCAAAT 1740

Qy   1741 GAAACTTTGACCTTTGAGGATGGCATGAACTTAAGGAATATGTGTAAAGGAGCAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GAAACTTTGACCTTTGAGGATGGCATGAACTTAAGGAATATGTGTAAAGGAGCAT 1800

Qy   1801 GGAGATTATACAGACAAAGCGATTTGAAAAACTTCACTGCCCAGAAGCAGGGTTTTCCACG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GGAGATTATACAGACAAAGCGATTTGAAAAACTTCACTGCCCAGAAGCAGGGTTTTCCACG 1860

Qy   1861 CAGACTGTAGCTGCTGTGGGAAACAGGAGGCAGTGGATGGAGAGCGCCTCAGACTCTG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CAGACTGTAGCTGCTGTGGGAAACAGGAGGCAGTGGATGGAGAGCGCCTCAGACTCTG 1920

Qy   1921 CTGCAGATGATGGCAGTGGCCGACATCACCTCCACCTGCCCCACGGGGCCTGACAGTGAG 1980
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Db   1921 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          CTGCAGATGATGGCAGTGGCGACATCACCTCCACCTCCACCTGCCCCACGCGGCCTGACAGTGAG 1980

Qy   1981 TCTGTGCTTAGCGTCAGTCGTCAGGAAGGGAAGACCAAGGACCCGTACAGCCCAGTGCTC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TCTGTGCTTAGCGTCAGTCGTCAGGAAGGGAAGACCAAGGACCCGTACAGCCCAGTGCTC 2040

Qy   2041 ATCCTGATGTGA 2052
          ||||||||||||
Db   2041 ATCCTGATGTGA 2052

RESULT 2
ABK12426
ID   ABK12426 standard; cDNA; 2240 BP.
XX
AC   ABK12426;
XX
DT   18-JUN-2002 (first entry)
XX
DE   Novel human protein ORF and flanking cDNA sequence #1.
XX
KW   Novel human protein; NHP; serine-threonine kinase;
KW   calcium/calmodulin-dependent kinase; myosin light chain kinase;
KW   biological disorder; gene; ss.
XX
OS   Homo.sapiens.
XX
PN   WO200218555-A2.
XX
PD   07-MAR-2002.
XX
PF   28-AUG-2001; 2001WO-US026776.
XX
PR   31-AUG-2000; 2000US-0229280P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Friddle CJ, Hilbun E, Nepomnichy B, Hu Y;
XX
DR   WPI; 2002-292200/33.
XX
PT   Novel polynucleotide encoding novel human protein sharing structural
PT   similarity with animal kinases e.g. serine-threonine, calcium/calmodulin-
PT   dependent, and myosin light chain kinases, useful as probes and primers.
XX
PS   Disclosure; Page 42; 46pp; English.
XX
CC   The present invention relates to the isolation of novel human proteins
CC   (NHPs) and the polynucleotide sequences encoding them. The NHPs of the
CC   invention are kinase proteins and share structural similarity to serine-
CC   threonine, calcium/calmodulin-dependent, and myosin light chain kinases.
CC   The sequences of the invention are useful for treating biological
CC   disorders. The polynucleotide sequences encoding the kinase proteins can
CC   be used as primers and probes. The sequences are also useful for
CC   identifying mutations associated with a particular disease and also in a
CC   prognostic or diagnostic assay. The present sequence represents NHP ORF
CC   (open reading frame) and flanking cDNA sequence #1
XX
SQ   Sequence 2240 BP; 749 A; 430 C; 515 G; 546 T; 0 U; 0 Other;

Query Match         100.0%;  Score 2052;  DB 6;  Length 2240;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 2052;   Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy     1 ATGGATAAGTACGATGTGATTAAGGCCACTGTGTCTTCGGGAAAGCATACTTA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   105 ATGGATAAGTACGATGTGATTAAGGCCACTGTGTCTTCGGGAAAGCATACTTA 164

Qy    61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   165 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 224
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Qy   121 CCCATACAAGAAAAGAGAGCTTCAAAGAAGAAGAGTGATTCTTCTGGAAAAGATGAAACAT 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225 CCCATACAAGAAAAGAGAGCTTCAAAGAAGAAGAGTGATTCTTCTGGAAAAGATGAAACAT 284

Qy   181 CCCACACATGTAGCCTTCTTCATTCAATTCATTTTCAAGAGATGGCAGGCGTGTTTATTGTAATG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285 CCCAACATTGTAGCCTTCTTCATTCAATTCATTTTCAAGAGATGGCAGGCGTGTTTATTGTAATG 344

Qy   241 GAATATTGTGATGGAGGGGATCCATGAAAAGAGTAACAATAGACAACGGGGTGTGTTATTT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 GAATATTGTGATGGAGGGGATCCATGAAAAGAGTAACAATAGACAACGGGGTGTGTTATTT 404

Qy   301 AGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTCTTCTGGAGGACTAAAACATATTCAT 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405 AGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTCTTCTGGAGGACTAAAACATATTCAT 464

Qy   361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGA 524

Qy   421 ATGTGGCAAAGTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525 ATGTGGCAAAGCTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 584

Qy   481 GCTCGAACTTGTATTGGAACACCTTACACCTGTCCCCAGAGATCTGTCGAATAAACCC 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   585 GCTCGAACTTGTATTGGAACACCTTACACCTGTCCCCAGAGATCTGTCGAATAAACCC 644

Qy   541 TACAACAATAAAACGGATATTTGGTCTTCTGGCTGTCGTCTTATATGAGCTCTGCACACTT 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   645 TACAACAATAAAACGGATATTTGGTCTTCTGGCTGTCGTCTTATATGAGCTCTGCACACTT 704

Qy   601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACAT 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   705 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACAT 764

Qy   661 TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   765 TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 824

Qy   721 CAAGTATCTCCTGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCCTTTTTTAGAG 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   825 CAAGTATCTCCTGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCCTTTTTTAGAG 884

Qy   781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGGAATTCAGTCACATGCTT 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   885 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGGAATTCAGTCACATGCTT 944

Qy   841 ATATGCAGAGCAGGAGCGGCCAGCTTCTCGACATGCTGGGGAAGGTGGTCCAGAAGTGTAAA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   945 ATATGCAGAGCAGGAGCGGCCAGCTTCTCGACATGCTGGGGAAGGTGGTCCAGAAGTGTAAA 1004

Qy   901 ATACAAAAGTGAGATTCAGGGAAAGTGCCACCAAGGATATCTGTGCCATTCAAGGATCAAG 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1005 ATACAAAAGTGAGATTCAGGGAAAGTGCCACCAAGGATATCTGTGCCATTCAAGGATCAAG 1064

Qy   961 AAAAGGAATGCTATATTGCATAGAAATGAAATGAATGCAGCACCAGCCACCAGCTGGAGCCCAGAAGGCC 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1065 AAAAGGAATGCTATATTGCATAGAAATGAAATGAATGCAGCACCAGCCACCAGCTGGAGCCCAGAAGGCC 1124

Qy  1021 AGATCTATAAAATGATAGAAGAAGACCCAAAATTGCTGCTGTCGTGCGACATTATGATTAT 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1125 AGATCTATAAAATGATAGAAGAAGACCCAAAATTGCTGCTGTCGTGCGACATTATGATTAT 1184

Qy  1081 TATTATGCTCAACTTGATATGCTGAGGAGGAGCCCACAAACCAAGTTATCACCCTATT 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1185 TATTATGCTCAACTTGATATGCTGAGGAGGAGCCCACAAACCAAGTTATCACCCTATT 1244

Qy  1141 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAAACGAGGCATGTCCATCCCCA 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1245 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAAACGAGGCATGTCCATCCCCA 1304

Qy  1201 AGTCAATGGCCTGCTGAGTCACCTTCAGAGAAAATTTGAAGCTCAACATATAAGTTGAAA 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 3
ADJ96571
ID   ADJ96571 standard; DNA; 2816 BP.
XX
AC   ADJ96571;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human Nim-A related protein kinase NEK5 DNA SeqID 28.
XX
KW   gene; ds; kinase; human; tyrosine protein kinase;
KW   serine/threonine protein kinase; PTK; STK; gene therapy; cancer;
KW   immune-related disease; cardiovascular disease; brain;
KW   neuronal associated disease; metabolic; inflammatory disorder;
KW   cytostatic; neuroprotective; immunomodulator; antiinflammatory;
KW   Nim-A related protein kinase; NEK5.
XX
OS   Homo sapiens.
OS   52.
XX
PN   WO2004006838-A2.
XX
PD   22-JAN-2004.
XX
PF   15-JUL-2003; 2003WO-US021730.
XX
PR   15-JUL-2002; 2002US-0395632P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Whyte D, Manning G, Caenepeel S;
XX
DR   WPI; 2004-122753/12.
DR   P-PSDB; ADJ96637.
XX
PT   New nucleic acid molecule encoding a kinase polypeptide, useful for
PT   preparing a composition for treating diseases or disorders; e.g., cancer,
PT   or neurological, immunological or inflammatory disorders.
XX
PS   Example 1; SEQ ID NO 28; 366pp; English.
XX
CC   This invention relates to a novel isolated, enriched or purified nucleic
CC   acid molecule that encodes a kinase polypeptide. Specifically, it relates
CC   to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
CC   as well as protein kinase-like enzymes. The present invention describes
CC   screening methods to identify agonists, antagonists and antibodies that
CC   can be used to modulate the activity or function of the mammalian kinase
CC   enzymes. As such, these compositions can be used for gene therapy
CC   purposes to treat diseases or disorders including cancer, immune-related
CC   diseases, cardiovascular disease, brain or neuronal associated disease,
CC   metabolic and inflammatory disorders. Accordingly, they exhibit
CC   cytostatic, neuroprotective, immunomodulator and antiinflammatory
CC   activities. This polynucleotide sequence is a human kinase DNA sequence
CC   of the invention.
XX
SQ   Sequence 2816 BP; 977 A; 508 C; 675 G; 656 T; 0 U; 0 Other;

Query Match             96.3%;  Score 1976.4;  DB 12;  Length 2816;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 1977;  Mismatches    0;  Conservative    0;  Indels    1;  Gaps    0;

Qy      1 ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGGATACTTA    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTA   377

Qy     61 GCTAAAGGGAAATCAGATAGCAAGGACACTGTGTCATAAAGATTTTGAAAAGATG            120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    378 GCTAAAGGGAAATCAGATAGCAAGGACACTGTGTCATGAAAGATCAATTTTGAAAAGATG      437

Qy    121 CCCATACAAGAAAGAAGAAGTTCAAGAAAGAAGTGATTCTTCTGGGAAAGATGAAACAT       180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438 CCCATACAAGAAAGAAGAAGTTCAAGAAAGAAGTGATTCTTCTGGGAAAGATGAAACAT      497

Qy    181 CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGAGAATGGCAGGCTGTTTATTGTAATG      240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    498 CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGAGAATGGCAGGCTGTTTATTGTAATG      557

Qy    241 GAATATTGTGATGGAGGGGATCTCATGAAAAGATCAATAGAACACGGGGTGTGTTATTT       300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    558 GAATATTGTGATGGAGGGGATCTCATGAAAAGATCAATAGAACACGGGGTGTGTTATTT      617

Qy    301 AGTGAAGATCAGAATCCTCGGTTGGTTTGTACAGATTTCTAGGACTAAAACATATTCAT       360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618 AGTGAAGATCAGAATCCTCGGTTGGTTTGTACAGATTTCTAGGACTAAAACATATTCAT      677

Qy    361 GACACGGAAGATATTACACACGGGACATAAAAAGTCCAGAACAATTTTTCTTAGCAAGAACGGA   420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1305 AGTCAATGGCCTGCTGAGTGACCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGTGAAA  1364
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1261 GTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA      1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1365 GTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA     1424

Qy   1321 GAGCTAAGAAGTAATGGAGAAGAGCCTAGATTCCAGGAGTTCAGGAAAAACGAA            1380
          ||||||||||||||||||||||||||||||||||||||||
Db   1425 GAGCTAAGAAGTAATGGAGAAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAAAAACGAA     1484

Qy   1381 ATGAAGAACACAGAATATTGGAGCAGTTAGAGGAAATACGGCCAACAGTACCACAATGAC      1440
          ||||| ||||||||  |||||||||||||||||||||||||||||||||||||||||||||
Db   1485 ATGAGGACACAGGGAATATTGGAGCAGTTAGAGGAAATACGGCCAACAGTACCACAATGAC    1544

Qy   1441 ATGAAAGAAATTAGAAAGAAGATGGGGGAGAGAACCAGAGGAGAACTCAAAAATAAGTCAT     1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1545 ATGAAAGAAATTAGAAAGAAGATGGGGGAGAGAACCAGAGGAGAACTCAAAAATAAGTCAT    1604

Qy   1501 AAAACCTATTTGGTGCAGGACATTGAAGAAGAGTAACCTGCCTGTCCATCAAGATGCATC      1560
          ||||||||||||||||||||||| |||||||||||||||||||||||||| |||||||||
Db   1605 AAAACCTATTTGGTGCAGGACAATTGAAGAAGAGTAACCTGCCTGTCCATCCAGATGCATC    1664

Qy   1561 GCACCTGTGCAGGACATTGAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAACAAGGAA   1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1665 GCACCTGTGCAGGACATTGAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAACAAGGAA  1724

Qy   1621 AGTAAAAATCCAGAACAGAAAATATAAAGCTAAGAAGGGGTAAAATTGAAATTAATTA       1680
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   1725 AGTAAAAATCCAGAACAGACAATATAAAGCTAAGAAGGGGTAAAATTGAAATTAATTA      1784

Qy   1681 GACAAAGTGTATTTCTGATGAAAACATCCTCCAAGAGGAGGCAATGGCAATGGGATATACCAAAT 1740
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1785 GACAAATGTATTTCTGATGAAAACATCCTCCAAGAGGAGGCAATGGCAATGGGATATACCAAAT  1844

Qy   1741 GAAACTTTGACCTTGAGGATGGCATGAAGGAGTTTAAGGAATTGAAATGTGTAAAGGAGCAT    1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1845 GAAACTTTGACCTTGAGGATGGCATGAAGGAGTTTAAGGAATTGAAATGTGTAAAGGAGCAT   1904

Qy   1801 GGAGATTATACAGACAAAGCATTTGAAAAACTTCACTGCCCAGAGCAGGGTTTCCACG        1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1905 GGAGATTATACAGACAAAGCATTTGAAAAACTTCACTGCCCAGAGCAGGGTTTCCACG       1964

Qy   1861 CAGACTGTGAGCTGCTGTGTGGGAAACAGGAGGCCAGTGGGATGGGAGGAGCGGCCGCCTCTG   1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1965 CAGACTGTGAGCTGCTGTGTGGGAAACAGGAGGCCAGTGGGATGGGAGGAGCGGCCGCCTCTG  2024

Qy   1921 CTGCAGATGATGGCAGTGCCAGTGGCCGACATCACCTCCACCCCACGGGGCCTGACAGTGAG    1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2025 CTGCAGATGATGGCAGTGCCAGTGGCCGACATCACCTCCACCCCACGGGGCCTGACAGTGAG   2084

Qy   1981 TCTGTGCTTAGGGTCAGTCGTCAGGAAGGGAAGGACCAAGGACCCGTACAGCCCAGTGCTC    2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085 TCTGTGCTTAGGGTCAGTCGTCAGGAAGGGAAGGACCAAGGACCCGTACAGCCCAGTGCTC   2144

Qy   2041 ATCCTGATGTGA     2052
          ||||||||||||
Db   2145 ATCCTGATGTGA    2156
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Db   1758 ATGAAGAGAAATTAGAAGAAGATGGGAGAGAACCAGAGGAGGAGAACTCAAAAATAAGTCAT 1817

Qy   1501 AAAACCTATTTGGTGAAGAAGAGTAACCTGCTGTCCATCAAGATGCATCTGAGGGACGAA 1560
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1818 AAAACCTATTTGGTGAAGAAGAGTAACCTGCCTGTCCATCAAGATGCATCTGAGGGGAGAA 1877

Qy   1561 GCACCTGTGCAGGACATTGAAAAAGACTTGAAACAAATGAAGGCTTCAGAACACAAAGGAA 1620
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1878 GCACCTGTGCAGGACATTGAAAAAGACTTGAAACAAATGAAGGCTTCAGAACACAAAGGAA 1937

Qy   1621 AGTAAAAATCCAGAACACAGAAATATAAAGCTAAGAAGGGGTAAAATTTGAAATTAATTTA 1680
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1938 AGTAAAAATCCAGAACACAGAAATATAAAGCTAAGAAGGGGTAAAATTTGAAATTAATTTA 1997

Qy   1681 GACAAAATGTATTTCTGATGAAAACATCCTCCAAGAGAGAGAGGCAATGATATACCAAAT   1740
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1998 GACAAAATGTATTTCTGATGAAAACATCCTCCAAGAGAGGAGGAGGCAATGATATACCAAAT 2057

Qy   1741 GAAACTTTGACCTTGAGGATGCATGAAGTTTAAGAAGTTAAGGAATATGAATGTGTAAAGGAGCAT 1800
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2058 GAAACTTTGACCTTGAGGATGGCATGAAGTTTAAGGAATATGAATGTGTAAAGGAGCAT 2117

Qy   1801 GGAGATTATACAGACAAAGCATTGAAAAACTTCACTGCCCAGAAGCAGGGGTTTTCCACG   1860
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2118 GGAGATTATACAGACAAAGCATTGAAAAACTTCACTGCCCAGAAGCAGGGGTTTTCCACG   2177

Qy   1861 CAGACTGTAGCTGCTGCTGTGGGAAACAGGAGGCAGTGGGATGGAGGAGCGCCTCAGACTCTG 1920
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2178 CAGACTGTAGCTGCTGCTGTGGGAAACAGGAGGCAGTGGGATGGAGGAGCGCCTCAGACTCTG 2237

Qy   1921 CTGCAGATGATGGCCAGTGCCGACATCACCTGCCCACCTGCCCACGGGGCCTGACAGTG   1978
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2238 CTGCAGATGATGGCAGTGCCGACATCACCTGCCCACCTGCCCACGGGGCCTGACAATG   2295

```
RESULT 4
ABK12425
ID   ABK12425 standard; cDNA; 1965 BP.
XX
AC   ABK12425;
XX
DT   18-JUN-2002  (first entry)
XX
DE   cDNA encoding novel human kinase protein #2.
XX
KW   Novel human protein; NHP; serine-threonine kinase; brain;
KW   calcium/calmodulin-dependent kinase; myosin light chain kinase;
KW   biological disorder; spleen; placenta; chromosome 6; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..1965
FT                  /*tag= a
FT                  /product= "Human kinase protein #2"
XX
PN   WO200218555-A2.
XX
PD   07-MAR-2002.
XX
PF   28-AUG-2001; 2001WO-US026776.
XX
PR   31-AUG-2000; 2000US-0229280P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Friddle CJ, Hilbun E, Nepomnichy B, Hu Y;
XX
DR   WPI; 2002-292200/33.
DR   P-PSDB; AAU77929.
XX
PT   Novel polynucleotide encoding novel human protein sharing structural
PT   similarity with animal kinases e.g. serine-threonine, calcium/calmodulin-
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Db   678 GACAGGAAGAGATATTACACAGGAGCATAAAAGCTTCAGAACACATTTTCTTAGCAAGAACGGA 737

Qy   421 ATGGTGGCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT   480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   738 ATGGTGGCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT   797

Qy   481 GCTCGAACTTGTATTGGAACACACTTACTACCTGTCCCCAGAGATCGTCTCAGAATAAACCC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   798 GCTCGAACTTGTATTGGAACACACCTTACTACCTGTCCCCAGAGATCGTCTCAGAATAAACCC 857

Qy   541 TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTCGTGTTATATGAGCTCTGCACACTT 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   858 TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTCGTGTTATATGAGCTCTGCACACTT 917

Qy   601 AAACATCCTTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAAGCACAT   660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   918 AAACATCCTTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAAGCACAT   977

Qy   661 TTTGCCCCAATATCCTCCGGGGTTTCTCGTGAGCTTCCTTGATATCCTCAGCTCTT   720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   978 TTTGCCCCAATATCCTCCGGGGTTTCTCGTGAGCTTCCTTGATATCTCAGCTCTT   1037

Qy   721 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTAGAG   780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTAGAG   1097

Qy   781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGTCACATGCTT   840
            |||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT 1157

Qy   841 ATATGCAGGAGCAGGAGCGCCAGCTTCTCGACATGCTCGGAGGTGGTCCAGAAGTGTAAA 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 ATATGCAGGAGCAGGAGCGCCAGCTTCTCGACATGCTCGGAGGTGGTCCAGAAGTGTAAA 1217

Qy   901 ATACAAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATCAAGGATATCTGTGCCAATT 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 ATACAAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATCAAGGATATCTGTGCCAATT 1277

Qy   961 AAAAGGAATGCTATATTGCATAGAAATGAATGGAGACCACCAGCTGGAGCCCAGAAGGCC 1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1278 AAAAGGAATGCTATATTGCATAGAAATGAATGGAGACCACCAGCTGGAGCCCAGAAGGCC 1337

Qy   1021 AGATCTATAAAAATGATAGAAAGACCCAAAATTGCTCGTCTGTGGGACATTATGATTAT 1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 AGATCTATAAAAATGATAGAAAGACCCAAAATTGCTCGTCTGTGTGGGACATTATGATTAT 1397

Qy   1081 TATTATGTCAACTTGATATGCTGAGGAGGAGCCCCAAACCAAGTTATCACCCCTATT 1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 TATTATGTCAACTTGATATGCTGAGGAGGAGCCCAAAACCAAGTTATCACCCTATT   1457

Qy   1141 CCTCAAGAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCATGGCCATCCCCA 1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1458 CCTCAAGAAATAACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCATGGTCATCCCCA   1517

Qy   1201 AGTCAATGGCTGCTGCTGAGTACTTCAGAGAAATTGAGCTCAACAATAAGTTGAAA   1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1518 AGTCAATGGCCTGCTGCTGAGTACTTCAGAGAAATTGAGCTCAACAATAAGTTGAAA   1577

Qy   1261 GTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGGCCAAATTACAACCAGAGACAA 1320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1578 GTGGGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGGCCAAATTACACCAGAGACACA 1637

Qy   1321 GAGCTAAGAGAGTAATGGAAGAGAGCCTAGATTCCAGGAGACTGCCATTTAGGAAAAACGAA 1380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1638 GAGCTAAGAGAGTAATGGAAGAGAGCCTAGATTCCAGGAGACTGCCATTTAGGAAAAAACGAA 1697

Qy   1381 ATGAAGGAACAGGAATATTGGAAGCAGTTAGAGGAAATACGGCCAACAATGAC   1440
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1698 ATGAAGGAACAGGAATATTGGAAGCAGTTAGAGGAAATACGCCAACAGTACCAAATGAC   1757

Qy   1441 ATGAAGAGAAATTAGAAGAAGATGGGAGAGAACCAGAGGAGGAGAACTCAAAAATAAGTCAT   1500

PT dependent, and myosin light chain kinases, useful as probes and primers.
XX
PS Disclosure; Page 39-40; 46pp; English.
XX
CC The present invention relates to the isolation of novel human proteins
CC (NHPs) and the polynucleotide sequences encoding them. The NHPs of the
CC invention are kinase proteins and share structural similarity to serine-
CC threonine, calcium/calmodulin-dependent, and myosin light chain kinases.
CC The sequences of the invention are useful for treating biological
CC disorders. The polynucleotide sequences encoding the kinase proteins can
CC be used as primers and probes. The sequences are also useful for
CC identifying mutations associated with a particular disease and also in a
CC prognostic or diagnostic assay. The present sequence encodes human
CC protein kinase #2 which is expressed in a broad range of human tissues
CC such as brain, spleen, and placenta. The gene encoding protein kinase #2
CC is located on chromosome 6
XX
SQ Sequence 1965 BP; 658 A; 377 C; 458 G; 472 T; 0 U; 0 Other;

Query Match   91.0%; Score 1868; DB 6; Length 1965;
Best Local Similarity   95.8%; Pred. No. 0;
Matches 1965; Conservative   0; Mismatches   0; Indels 87; Gaps 1;

```
Qy     1 ATGGATAAGTACGATGTGATTAAGGACATGGCCATCGGCAAGGTGCCTTCGGCAAGCATACTTA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGATAAGTACGATGTGATTAAGGACATGGCCATCGGCAAGGTGCCTTCGGCAAGCATACTTA 60

Qy    61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 120

Qy   121 CCCATACAAGAAAAAGAGAGCTTCAAAGAAAAGAGTGATTCTTCTGGAAAAGATGAAACAT 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCCATACAAGAAAAAGAGAGCTTCAAAGAAAAGAGTGATTCTTCTGGAAAAGATGAAACAT 180

Qy   181 CCCAACATTGTAGCCTTCTCAATTCATTCAAGAAAGGACATAATAGACAACGGGGTGTTATTG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCCAACATTGTAGCCTTCTCAATTCATTCAAGAAAGGACATAATAGACAACGGGGTGTTATTG 240

Qy   241 GAATATTGTGATGGGAGGGGATCCATGAAAAGGACATAAAGAGACAACGGGGTGTGTTATTT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GAATATTGTGATGGGAGGGGATCCATGAAAAGGACATAAAGAGACAACGGGGTGTGTTATTT 300

Qy   301 AGTGAAGATCAGATCCTCGGTTGGTTTGTTGTACAGATTTCTACAGATAATATTCAT 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGTGAAGATCAGATCCTCGGTTGGTTTGTTGTACAGATTTCTACAGATAATATTCAT 360

Qy   361 GACAGGAAGAATATTACACAGGGACATAAAAGTCAGAACATTTTCTTAGCAAGAACGGA 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACAGGAAGAATATTACACAGGGACATAAAAGTCAGAACATTTTCTTAGCAAGAACGGA 420

Qy   421 ATGGTGGCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGTGGCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480

Qy   481 GCTCGAACTTGTATTGGAACACACTTACTACCTGTCCCCAGAGATCTGTCGAGAATAAACCC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCTCGAACTTGTATTGGAACACACTTACTACCTGTCCCCAGAGATCTGTCGAGAATAAACCC 540

Qy   541 TACAACAATAAAACGGATATTGGTCTTGGTCTTGCGTCTTTATATGAGCTCTGCACACTT 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TACAACAATAAAACGGATATTGGTCTTGGTCTTGCGTCTTTATATGAGCTCTGCACACTT 600

Qy   601 AAAACTCCTTTGAGGGTAACAACTTACAGCAGTCTTCGAAGATTGGTCAAGGACAT 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AAAACTCCTTTGAGGGTAACAACTTACAGCAGTCTTCGAAGATTGGTCAAGGACAT 660

Qy   661 TTTGCCCAATATCTCCGGGGTTTCGTGAGTCCATTCCTTGATATCTCAGTTCTTT 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TTTGCCCAATATCTCCGGGGTTTCGTGAGTCCATTCCTTGATATCTCAGTTCTTT 720

Qy   721 CAAGTATCTCCTGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTGAGAG 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 CAAGTATCTCCTGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTGAGAG 780

Qy   781 AATCTTATTCCCAAATATTTGACTCCTGAGTCATTCAGGAAGAATTCAGTCACATGCTT 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 AATCTTATTCCCAAATATTTGACTCCTGAGTCATTCAGGAAGAATTCAGTCACATGCTT 840

Qy   841 ATATGCAGAGCAGGAGCGGCCAGCTTCTCGACATGCTGGGAAGGTGGTCCAGAAGTGTAAA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ATATGCAGAGCAGGAGCGGCCAGCTTCTCGACATGCTGGGAAGGTGGTCCAGAAGTGTAAA 900

Qy   901 ATACAAAAAGTGAGATTCCAGGGAAAGTGCCACCAAGATCAAGGATATCTGTGCCAATT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATACAAAAAGTGAGATTCCAGGGAAAGTGCCACCAAGATCAAGGATATCTGTGCCAATT 960

Qy   961 AAAAGGAATGCTATATTGCATAGAAATGATGAGACACCAGTTGGAGCCCAGAAGCCCAGAAGGCC 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 AAAAGGAATGCTATATTGCATAGAAATGATGAGACACCAGTTGGAGCCCAGAAGCCCAGAAGGCC 1020

Qy  1021 AGATCTATAAAAATGATAGAAGACCCAAAATTGCTCGTCTGTGGGACATTATGATTAT 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 AGATCTATAAAAATGATAGAAGACCCAAAATTGCTCGTCTGTGGGACATTATGATTAT 1080

Qy  1081 TATTATGCTCAACTTGATATGCTGAGGAGAGAGCCCACAAACCAAGTTATCACCCTATT 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TATTATGCTCAACTTGATATGCTGAGGAGAGAGCCCACAAACCAAGTTATCACCCTATT 1140

Qy  1141 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCATGTCCATCCCCA 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCATGTCCATCCCCA 1200

Qy  1201 AGTCAATGGCCTGCTGAGTACCTGTCGAGAAAATTTGAAGCTCAACAATATAAGTGAAA 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 AGTCAATGGCCTGCTGAGTACCTGTCGAGAAAATTTGAAGCTCAACAATATAAGTGAAA 1260

Qy  1261 GTGGAGAAGCAATTGGTCTTCGTCCGAGCCAAATTACAACCAGAGACAA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GTGGAGAAGCAATTGGTCTTCGTCCGAGCCAAATTACAACCAGAGACAA 1320

Qy  1321 GAGCTAAGAGTAATGAGAAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAAAAACGAA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 GAGCTAAGAGTAATGAGAAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAAAAACGAA 1380

Qy  1381 ATGAAGGACAGAGATATTGGGGAAGAATACGCCAACAGTACCACAATGAC 1440
         ||||||||||||
Db  1381 ATGAAGGAAC                                         1390

Qy  1441 ATGAAAGAAATTAGAAAGAAGATGGGGAGGAGAACTCAAAAATAAGTCAT 1500
         --------------------------------------------------
Db  1391 --------------------------------------------------  1413
                                                   AGGAGAACTCAAAAATAAGTCAT 1413

Qy  1501 AAAACCTATTTGGTGAAGAGAGTAACCTGCCATCAAGATGCATCTCGAGGGAGAA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1414 AAAACCTATTTGGTGAAGAGAGTAACCTGCCATCAAGATGCATCTCGAGGGAGAA 1473

Qy  1561 GCACCTGTCGAGAAGCATTGAAAGAACTTGAAACAAATGAGGCTTCAGAACAAAGGAA 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1474 GCACCTGTCGAGAAGCATTGAAAGAACTTGAAACAAATGAGGCTTCAGAACAAAGGAA 1533

Qy  1621 AGTAAAAATCCAGAACAGAGAAATATAAAGCTAAGAGGGGGTAAAATTTGAAATTAATTTA 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1534 AGTAAAAATCCAGAACAGAACAGAAATATAAAGCTAAGAGGGGGTAAAATTTGAAATTAATTTA 1593

Qy  1681 GACAAATGTATTTCTGATGAAAAACATCCTCCAAGAGGAGAGGCAATGAATGTCAATATACCAAAT 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1594 GACAAATGTATTTCTGATGAAAAACATCCTCCAAGAGGAGAGGCAATGAATGTCAATATACCAAAT 1653

Qy  1741 GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGTAAGTGTAAGGACAT 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1654 GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGTAAGTGTAAGGACAT 1713

Qy  1801 GGGATTATACAGACAAAGACATTTGAAAAACTTCACTGCCCAGAAGCAGCAGGGTTTTCCACG 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1714 GGGATTATACAGACAAAGACATTTGAAAAACTTCACTGCCCAGAAGCAGCAGGGTTTTCCACG 1773
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Qy   1861  CAGACTGTAGCTGCTGTGGGAAACAGGAGGCAGTGGGATGGAGAGGCGCCTCAGACTCTG  1920
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   1774  CAGACTGTAGCTGCTGTGGGAAACAGGAGGCAGTGGGATGGAGAGCCGCCTCAGACTCTG  1833

Qy   1921  CTGCAGATGATGGCAGTGGCCGACATCACCTCGCCCACCTGCCCCACGGGGCCTGACAGTGAG  1980
            ||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db   1834  CTGCAGATGATGGCAGTGGCCGACATCACTCCACCTGCCCCACGGGGCCTGACAGTGAG  1893

Qy   1981  TCTGTGGCTTAGCGGTCAGTGCTCAGGAAGGAAGGACCAAGGAAGACCAAGGACCCGTACAGCCCAGTGCTC  2040
            |||||| |||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1894  TCTGTGCTTAGCGGTCAGTCGTCAGGAAGGAAGGACCAAGGAAGACCAAGGACCCGTACAGCCCAGTGCTC  1953

Qy   2041  ATCCTGATGTGA  2052
            ||||||||||||
Db   1954  ATCCTGATGTGA  1965
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RESULT 5
ABS57149
ID   ABS57149 standard; cDNA; 2370 BP.
XX
AC   ABS57149;
XX
DT   04-FEB-2003 (first entry)
XX
DE   Human cDNA encoding a serine/threonine kinase.
XX
KW   Human; ss; gene; serine/threonine kinase; lung carcinoma; chromosome 13.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   12..1934
FT   /tag= a
FT   /product= "Ser/Thr kinase"
XX
PN   WO200281727-A2.
XX
PD   17-OCT-2002.
XX
PF   02-APR-2002; 2002WO-US010156.
XX
PR   03-APR-2001; 2001US-00824583.
PR   05-JUN-2001; 2001US-00873404.
XX
PA   (PEKE) PE CORP NY.
XX
PI   Webster M, Yan C, Di Francesco V, Beasley EM;
XX
DR   WPI; 2003-058562/05.
DR   P-PSDB; ABG72000.
XX
PT   Novel human kinase protein expressed in lung carcinoma and placenta is
PT   useful to diagnose and treat diseases and disorders associated with
PT   expression or activity of the protein.
XX
PS   Claim 22; Fig 1A; 101pp; English.
XX
CC   The invention relates to an isolated human kinase peptide of the
CC   serine/threonine, an allelic variant or orthologue, and encoded by a
CC   nucleic acid that hybridises under stringent conditions with the cDNA and
CC   gene sequences appearing as ABS57149 and ABS57150, or a fragment
CC   comprising at least 10 contiguous amino acids. Also included are an
CC   antibody that selectively binds to the kinase, a gene chip comprising the
CC   nucleic acids, a transgenic non human animal comprising the nucleic
CC   acids, a nucleic acid vector comprising the nucleic acids, a host cell
CC   containing the vector and expressing the kinase, identifying a
CC   modulator/binding agent of the kinase (comprising contacting the peptide
CC   with an agent and determining if the agent has modulated function), The
CC   expression or activity of the peptide or formed a complex with it), The
CC   molecules of the invention are useful to diagnose and treat a disorder
CC   characterised by aberrant expression of the protein (e.g. lung
CC   carcinoma). Agents which modulate the function or activity of the protein
CC   are useful to treat diseases or disorders mediated by human kinase
CC   protein. The gene for encoding the novel kinase is located on chromosome
CC   13. The present sequence is the cDNA encoding the novel human kinase
XX
SQ   Sequence 2370 BP; 796 A; 550 G; 456 C; 568 T; 0 U; 0 Other;

Query Match   80.6%; Score 1654; DB 8; Length 2370;
Best Local Similarity   94.5%; Pred. No. 0;
Matches 1763; Conservative 0; Mismatches 10; Indels 93; Gaps 1;

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Qy    1  ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTA   60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   12  ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTA   71

Qy   61  GCTAAAGGGAAATCAGATAGCAAGCACACTGTGTCATAAAAGATCAATTTGAAAAGATG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   72  GCTAAAGGGAAATCAGATAGCAAGCACACTGTGTCATAAAAGATCAATTTGAAAAGATG  131

Qy  121  CCCATACAAGAAAAAGAAGCTTCAAAGAAGAAGTGATTCTTCTGGAAAGAATGAAACAT  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  132  CCCATACAAGAAAAAGAAGCTTCAAAGAAGAAGTGATTCTTCTGGAAAGAATGAAACAT  191

Qy  181  CCCAACATTGTAGCCTTCTTCAATCATTCATTCAAGAGAATGGCAGGCTGTTATTGTAATG  240
         ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db  192  CCCAACATTGTAGCCTTCTTCAATCATTCATTCAAGAGAATGGCAGGCTGTTTATTGTAATG  251

Qy  241  GAATATTGTGATGGAGGGGATCTCATGAAAGATCAATAGACAACGGGGTGTGTATTT  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252  GAATATTGTGATGGAGGGGATCTCATGAAAGATCAATAGACAACGGGGTGTGTATTT  311

Qy  301  AGTGAAGATCAGATCCTCGGTTGGTTTGTATACAGATTTCTCAGGACTAAAACATATTCAT  360
         ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  312  AGTGAAGATCAGATCCTCGGTTGGTTTGTTACAGATTTCTCAGGACTAAAACATATTCAT  371

Qy  361  GACAGGAAGAGATATTACACAGGGACATAAAAGTCAGAACATTTTCTTAGCAAGAACGGA  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  372  GACAGGAAGAGATATTACACAGGGACATAAAAGTCAGAACATTTTCTTAGCAAGAACGGA  431

Qy  421  ATGGTGGCAAAGCTTGGGACTTGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  432  ATGGTGGCAAAGCTTGGGACTTGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  491

Qy  481  GCTCGAACTTGTATTGAACACCTTACCTGTCCCCAGAGATCTGTCAGAATAAACCC  540
         ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db  492  GCTCGAACTTGTATTGGAACACCTTACCTGTCCCCAGAGATCTGTCAGAATAAACCC  551

Qy  541  TACAACAATAAAACGGATATTGGTCCTTGGTCGTGTGTCTTATATGAGCTCTGCACACTT  600
         ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  552  TACAACAATAAAACGGATATTGGTCTCTTGGTCGTGTGTCTTATATGAGCTCTGCACACTT  611

Qy  601  AAACATCCTTTGAGGGTAACAACTTACAGACAGCTGGTTCTGAAGATTGTCAAGCACAT  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  612  AAACATCCTTTGAGGGTAACAACTTACAGACAGCTGGTTCTGAAGATTGTCAAGCACAT  671

Db  661  TTTGCCCAATATCTCCGGGGTTTCTCCGTGAGCTCCATTCCATTTGATATCTCAGCTCTT  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  672  TTTGCCCAATATCTCCGGGGTTTCTCCGTGAGCTCCATTCCATTTGATATCTCAGCTCTT  731

Qy  721  CAAGTATCCTCGAGACGACACCATCCATAAATTCCATTTGAAAAGGCCCCTTTTTAGAG  780
         |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  732  CAAGTATCCTCGAGACGACCATCCATAAATTCCATTTGAAAAGGCCCCTTTTTAGAG  791

Qy  781  AATCTTATTCCCAAATATTGACTCCTGAGGTTCATTCAGGAGAATTCAGTCACATGCTT  840
         |||||||||||||||||||||||||||||| |||||||||||||||||||||||||| |
Db  792  AATCTTATTCCCAAATATTGACTCCTGAGGTCATTCAGGAGAATTCAGTCACATGTT  851

Qy  841  ATATGCAGGAGGAGGCCAGTCCGACATGCTGGAGGTGGTCCAGAAGTGTAAA  900
         |||||||||||||||||    |||||||||||||||||||||||||||||||
Db  852  ATATGCAGGAGGAGGCCCAGCTTCTCGACATGCTGGAGGTGGTCCAGAAGTGTAAA  911

Qy  901  ATACAAAAGTGAGATTCCAGGGAAGTGCCCACCAAGATCAAGGATATCTGTGCCAATT  960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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DT   12-SEP-2001  (first entry)
XX
DE   Polynucleotide sequence encoding human protein kinase #45.
XX
KW   Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW   metabolic disorder; immune related disease; neurological disorder;
KW   neurodegenerative disorder; immune related disease; inflammatory disorder; infectious disease;
KW   reproductive disorder; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138503-A2.
XX
PD   31-MAY-2001.
XX
PF   22-NOV-2000; 2000WO-US032085.
XX
PR   24-NOV-1999;  99US-0167482P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD,  Whyte D,  Manning G,  Sudarsanam S,  Martinez R;
PI   Flanagan P,  Clary D;
XX
DR   WPI; 2001-343950/36.
DR   P-PSDB; AAU03545.
XX
PT   Nucleic acids encoding human kinase polypeptides, useful for preventing
PT   diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT   neuronal-associated diseases, and microbial infections.
XX
PS   Example 1; Fig 1; 433pp; English.
XX
CC   AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
CC   protein kinases have been identified as members of the tyrosine or
CC   serine/threonine kinase (PTK and STK) families. The polynucleotides
CC   encoding protein kinases and the polypeptides may be used in the
CC   prevention, diagnosis and treatment of diseases associated with
CC   inappropriate kinase expression. For example, they may be used to treat
CC   cancers (especially cancers of haematopoietic origin), cardiovascular
CC   disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC   immune related diseases (e.g. rheumatoid arthritis), neurological
CC   disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC   Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC   disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC   Additionally, polynucleotides encoding protein kinases may be used for
CC   gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC   polypeptides may be used as antigens in the production of antibodies
CC   against the protein kinases and in assays to identify modulators of
CC   protein kinase expression and activity
XX
SQ   Sequence 1947 BP; 638 A; 357 C; 455 G; 497 T; 0 U; 0 Other;
```

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Query Match             71.6%;  Score 1469.6;  DB 4;  Length 1947;
Best Local Similarity   87.0%;  Pred. No. 0;
Matches  1721;  Conservative    0;  Mismatches   89;  Indels  168;  Gaps  3;

Qy         1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTCGGGAAAGCATACTTA 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTCGGGAAAGCATACTTA 60

Qy        61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCTCATAAAAGAGATCAATTTTGAAAGATG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCTCATAAAAGAGATCAATTTTGAAAGATG 120

Qy       121 CCCTACAAGAAAAAGAGCTTCAAGAAAGAAGAGTGATTCTTCTGGAAAGATGAAACAT 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CCCTACAAGAAAAAGAGCTTCAAGAAAGAAGAGTGATTCTTCTGGAAAGATGAAACAT 180

Qy       181 CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGATGGCAGGCTGTTTATTGTAATG 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGATGGCAGGCTGTTTATTGTAATG 240
```

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Db       912 ATACAAAAAGTGAGATTCCGGGGAAAGTGCCCACCAAGATCAAGGATATCTGTGCCAATT 971

Qy       961 AAAAGGAATGCTATATTGCATAGAAATGAAATGAATGAAGACCACCAGCCCAGAAGGCC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       972 AAAAGGAATGCTATATTGCATAGAAATGAAATGAATGAAGACCACCAGCCCAGAAGGCC 1031

Qy      1021 AGATCTATAAAAATGATGAGAAAGACCCAAATTGCTGCTGTGTCTGTGGACATTATGATTAT 1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1032 AGATCTATAAAAATGATGAGAAAGACCCAAATTGCTGCTGTGTCTGTGGACATTATGATTAT 1091

Qy      1081 TATTATGCTCAACTTGATATGTCTGAGGAGGAGAGCCCACAAACCAAGTTATCACCCTATT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1092 TATTATGCTCAACTTGATATGTCTGAGGAGGAGAGCCCACAAACCAAGTTATCACCCTATT 1151

Qy      1141 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAAACGAGGCATGGTCCATCCCA 1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1152 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAAACGAGGCATGTCCATCCCA 1211

Qy      1201 AGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAAA 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1212 AGTCAATGGCCTGCTGAGTACCTTCAGAGAAAATTTGAAGCTCAACAATATAAGTTGAAA 1271

Qy      1261 GTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA 1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1272 GTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA 1331

Qy      1321 GAGCTAAGAAGTAATGAGAGAGAGCCTAGATTCCAGGAGTCGCCATTTAGGAAAAACGAA 1380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1332 GAGCTAAGAAGTAATGAGAGAGAGCCTAGATTCCAGGAGTCGCCATTTAGGAAAAACGAA 1391

Qy      1381 ATGAAGGAACAGGAATATTGGAAGCAGTTAGAGGAATAACGCCAACAGTACCACAATGAC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db      1392 ATGAAGGAACAGGAATATTGGAAGCAGTTAGAGGAATAACGCCAACAGTACCTCAATGAC 1451

Qy      1441 ATGATAGAAGAGATGGGGAGAGAACCAGAGGAGAACTCAAAAATAAGTCAT 1500
             ||||| |||||||||||||||||||||||||||||||
Db      1452 ATGAAAGAGATTAGAAGAGATGGGGAGAGAACCAGAGGAGAACAAAAGGAGAACC------ 1488

Qy      1501 AAAACCTATTTGGTGAAGAAGTAACCTGCTGCTGTCCTGTCCATCAGATGCCATCGAGGGAGAA 1560
             -----------------------------------------
Db      1488 ------------------------------------------------------------ 1488

Qy      1561 GCACCTGTGCAGGACATTGAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGAA 1620
             --------|||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1489 --------AGGACATTGAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGAA 1538

Qy      1621 AGTAAAAATCCAGAACAACAGAACAGCATTTGAAAAATATAAAGGGGGTAAAATTTGAAATTAATTTA 1680
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1539 AGTAAAAATCCAGAACAACAGAACAGCATTTGAAAAATATAAAGGGGGTAAAATTTGAAATTAATTTA 1598

Qy      1681 GACAAATGTATTTCTGATGAAAAACATCCTCCAAGAGGAAGAGGCAATGGCAATATACCAAAAT 1740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1599 GACAAATGTATTTCTGATGAAAAACATCCTCCAAGAGGAAGAGGCAATGGCAATATACCAAAAT 1658

Qy      1741 GAAACTTTGACCTTGACGGATGGCATGAAGTTTAAGGAATATGAATGTGTAAAGGAGCAT 1800
             |||||||||||||||||||||||||||||||||||||||||||   |||||||||||||
Db      1659 GAAACTTTGACCTTGACGGATGGCATGAAGTTTAAGGAATATGTGTAAAGGAGCAT 1718

Qy      1801 GGAGATTATACAGACAAAGCATTTGAAAAAACTTCACTGCCCAGAAGCAGGGTTTTCCACG 1860
             |||||||||||||||||||||||||||||||||||||||||||||||||||   |  |||
Db      1719 GGAGATTATACAGACAAAGCATTTGAAAAAACTTCACTGCCCAGAAGCAGCATTTACAGAA 1778

Qy      1861 CAGACT 1866
             ||  ||
Db      1779 CTGACT 1784
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RESULT 6
AAS06745
ID   AAS06745 standard; cDNA; 1947 BP.
XX
AC   AAS06745;
XX
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241 Qy  GAATATTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATT   300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 Db  GAATATTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATTT  300

301 Qy  AGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTTCTTCTAGGACTAAAACATATTCAT  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 Db  AGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTTCTTCTAGGACTAAAACATATTCAT  360

361 Qy  GACAGGAAGATATTACACAGGGTAACAAAAGCTCAGAACACATTTCTTAGCAAGAACGGA  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 Db  GACAGGAAGATATTACACAGGGTAACAAAAGCTCAGAACACATTTCTTAGCAAGAACGGA  420

421 Qy  ATGGTGGCAAAGCTTGGGAGCTTTGGTATAGCAAGAGTCTGAATAATTCCATGGAACTT  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 Db  ATGGTGGCAAAGCTTGGGAGCTTTGGTATAGCAAGAGTCTGAATAATTCCATGGAACTT  480

481 Qy  GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCC  540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 Db  GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCC  540

541 Qy  TACAACAATAAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 Db  TACAACAATAAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT  600

601 Qy  AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTCGAAGATTGTCAAGCACAT  660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 Db  AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTCGAAGATTGTCAAGCACAT  660

661 Qy  TTTGCCCCAATATCTCCGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT  720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 Db  TTTGCCCCAATATCTCCGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT  720

721 Qy  CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAAGGCCCTTTTTAGAG  780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 Db  CAAGTATCTCCTCGAGACCGACCATCCATCAATAAATTCCATTTGAAAAAGGCCCTTTTTAGAG  780

781 Qy  AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT  821
        ||||||||||||||||||||||||||||||||||||
781 Db  AATCTTATTCCCAAATATTTGACTCCTGAGGTAAGTTTTGA----------------   821

822 Qy  --------GGTGACTGTTGTTGGATTTGGTGAGAGATTTCGGTTGCAGGTCCTTG  867

841 Qy  ATATGCAGAGCAGGAGCGGCCAGCTTCTCGACATGCTGGGAAGTGGTCCAGAGTGTAAA  900
        ||||||||||||||||||||||||||||||||||||||
868 Db  ACACGTGTGTTCGGTTCGGTTTAGGTGTGAGCCACTGCACCCGTGTATTATGGTTTTTAAA  927

901 Qy  ATACAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATCAAGGATATCTGTGCCAATT  960
        ||||||||||||||||||||||||
961 Db  AAAAGGAATGCTATATTGCATAGAAATGAATGAGACCACCAGCTGAGCCCAGAAGGCC  1020

961 Qy  AAAAGGAATGCTATATTGCATAGAAATGAATGAGACCACCAGCTGAGCCCAGAAGGCC  948
928 Db  AACATCCCCTCTTGTTTCTT----------------------------------   948

1021 Qy  AGATCTATAAAAATGATAGAAAGACCCAAAATTGCTGCTGTCTGTGGACATTATGATTAT  1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||
949 Db  ---CAGATAAAAATGATAGAAAGACCCAAAATTGCTGCTGTCTGTGGACATTATGATTAT  1005

1081 Qy  TATTATGTCAACTTGATATGCTGAGGAGGAGCCCACAAACCAAGTTATCACCCTATT  1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1006 Db  TATTATGTCAACTTGATATGCTGAGGAGGAGCCCACAAACCAAGTTATCATCCCTATT  1065

1141 Qy  CCTCAAGAAATACTGGAGTTGAGGATTACGGTCAGGAAACAGAGGCATGGTCATCCCCA  1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
1066 Db  CCTCAAGAAATACTGGAGTTGAGGATTACGGTCAGGAAACAGAGGCATGGTCATCCCCA  1125

1201 Qy  AGTCAATGGCCTGCTGAGTGACCTTGCTGAGAGAAAATTTGAAGTCAACATATAAGTTGAAA  1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1126 Db  AGTCAATGGCCTGCTGAGTGACCTTGCTGAGAGAAAATTTGAAGTCAACATATAAGTTGAAA  1185

1261 Qy  GTGGAGAAGCAATTGGGTCTTCGTCCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA  1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
1186 Db  GTGGAGAAGCAATTGGGTCTTCGTCCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA  1245

1321 Qy  GAGCTAAGAAGTAATGGAGAAGAGCCTAGAATTCCAGAGCTGCCATTTAGGAGAAAACGAA
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1246 Db  GAGCTAAGAAGTAATGGAGAAGAGCCTAGAATTCCAGAGCTGCCATTTAGGAGAAAACGAA  1305

1381 Qy  ATGAAGGAACAGGAATATTGGAAGCAGTAGAGGAGCAGTAGAGGAAATACGCCAACAGTACCACCAATGAC  1440
1306 Db  ATGAAGGAACAGGAATATTGGAAGCAGTAGAGGAGCAGTAGAGGAAATACGCCAACAGTACCACCAATGAC  1365

1441 Qy  ATGAAAGAAATTAGAAGAGATGGGGAGAAGAGGAGAACCAGAGGAGAACTCAAAAAAATAAGTCAT  1500
1366 Db  ATGAAAGAAATTAGAAGAGATGGGGAGAAGAGGAGAGAACCAG----------------  1402

1501 Qy  AAAACCTATTTGGTGAAGAGTAACCTGCCTGTCCATCAAGATGCATCTGAGGGAGAA  1560
1403 Db  ----------------------------------------------------------  1402

1561 Qy  GCACCTGTCGCAGGACATTGAAAAAGACTTCAGAAACAAATGAGGCTTCAGAACACAAAGGAA  1620
1403 Db  -------AGGACATTGAAAAAGACTTCAGAAACAAATGAGGCTTCAGAACACAAAGGAA  1452

1621 Qy  AGTAAAAATCCAGAACACAGAAATATAAAGCTAAGAAGGGGTAAAATTTGAAATTAATTTA  1680
1453 Db  AGTAAAAATCCAGAACACAGAAATATAAAGCTAAGAAGGGGTAAAATTTGAAATTAATTTA  1512

1681 Qy  GACAAATGTATTCTGATGAAAACATCCTCCAGAGGAGGAGCAATGGAATATGTGTAAAGGAGCAT  1740
1513 Db  GACAAATGTATTCTGATGAAAACATCCTCCAGAGGAGGAGCAATGGAATATGTGTAAAGGAGCAT  1572

1741 Qy  GAAACTTTGACCTTTGAGGATGGCATGAAAGCATTGAAAAACTTCACTGCCCGAAGCAGGGTTTTCACG  1800
1573 Db  GAAACTTTGACCTTTGAGGATGGCATGAAAGCATTGAAAAACTTCACTGCCCGAAGCAGGGTTTTCACG  1632

1801 Qy  GGAGATTATACAGACAAAGCATTGAAAAACTTCACTGCCCGAAGCAGGGTTTTCACG  1860
1633 Db  GGAGATTATACAGACAAAGCATTGAAAAACTTCACTGCCCGAAGCAGGGTTTTCACG  1692

1861 Qy  CAGACTGTAGCTCGTGTGGGAAACAGAGGCAGTGGGATGGGATGGGAGGAGCGCCTCAGACTCTG  1920
1693 Db  CAGACTGTAGCTCGTGTGGGAAACAGAGGCAGTGGGATGGGATGGGAGGAGCGCCTCAGACTCTG  1752

1921 Qy  CTTGCAGATGATGGCCAGTGCCGACATCGCCCCACCTGCCCCACTTGCCCACTGCGGGGGCCCTGACAGTG  1978
1753 Db  CTTGCAGATGATGGCCAGTGCCGACATCGCCCCACCTGCCCCACTTGCCCACTGCGGGGGCCCTGACAATG  1810
```

RESULT 7
AB259716

ID	AB259716	standard; DNA; 1896 BP.
XX		
AC	AB259716;	
XX		
DT	17-APR-2003 (first entry)	
XX		
DE	Human NEK-like serine/threonine protein kinase DNA # SEQ ID 1.	
XX		
KW	Human; NEK-like serine/threonine protein kinase; cytostatic; cardiant;	
KW	antiinflammatory; nootropic; neuroprotective; cancer; colon cancer;	
KW	cardiovascular disorder; diabetes; COPD; CNS disorder; gene; ds.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..1896
FT		/*tag= a
FT		/product= "NEK-like serine/threonine protein kinase"
XX		
PN	WO2003000903-A2.	
XX		
PD	03-JAN-2003.	
XX		
PF	24-JUN-2002; 2002WO-EP006948.	
XX		
PR	25-JUN-2001; 2001US-0300068P.	
PR	07-DEC-2001; 2001US-0336704P.	

XX
PA (FARB) BAYER AG.
XX
PI Xiao Y;
XX
DR WPI; 2003-184051/18.
DR P-PSDB; ABP71710.
XX
PT New polynucleotide encoding a NEK-like serine/threonine kinase
PT polypeptide useful for treating diseases associated with kinase
PT dysfunction, e.g. cardiovascular disorders, cancer such as colon cancer,
PT diabetes and CNS disorders.
XX
PS Claim 1 b; Fig 1; 149pp; English.
XX
CC The invention relates to a newly isolated polynucleotide encoding an NEK-
CC like serine/threonine protein kinase. The activity of the polynucleotide
CC and polypeptide of the invention may be described as cytostatic,
CC cardiant, antiinflammatory, nootropic and neuroprotective. The expression
CC vector and reagent of the invention are useful for the preparation of a
CC medicament for modulating the activity of an NEK-like serine/threonine
CC kinase in a disease, such as cancer (e.g. colon cancer) cardiovascular
CC disorder, diabetes, COPD or CNS disorder. The polypeptides may also be
CC used to identify compounds which may act as activators or inhibitors at
CC the enzyme's active site, to raise specific antibodies which can block
CC the enzyme and effectively reduce its activity, as a bait protein in a
CC two-hybrid or three-hybrid assay to identify other proteins which bind to
CC or interact with the human NEK-like serine/threonine kinase polypeptide
CC and modulate its activity, and for the immunisation of mammals. The
CC current sequence represents the human NEK-like serine/threonine protein
CC kinase encoding DNA
XX
SQ Sequence 1896 BP; 608 A; 360 C; 455 G; 473 T; 0 U; 0 Other;

Query Match   66.3%; Score 1359.8; DB 8; Length 1896;
Best Local Similarity 84.5%; Pred. No. 0;
Matches 1673; Conservative   0; Mismatches   82; Indels 224; Gaps 4;

Qy   1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCAAGTGCCTTCGGGAAGCATACTTA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCAAGTGCCTTCGGGAAGCATACTTA 60

Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAGAGATCAATTTGAAAAGATG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAGAGATCAATTTGAAAAGATG 120

Qy   121 CCCATACAAGAAAAGAAGCTTCAAAGAAGTGATTCTTCTGAAAAGAGTGAAACAT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCCATACAAGAAAAGAAGCTTCAAAGAAGTGATTCTTCTGAAAAGAGTGAAACAT 180

Qy   181 CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGAAGATGCAGGCTGTTTATTGTAATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCCAACAATTGTAGCCTTCTTCAATTCATTTCAAGAAGATGCAGGCTGTTTATTGTAATG 240

Qy   241 GAATATTGTGATGGAGGGGATCCATGGAGGGGATCAATAGACAATGACAACGGGGTGTGTATTT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GAATATTGTGATGGAGGGGATCCATGGAGGGGATCAATAGACAATGACAACGGGGTGTGTATTT 300

Qy   301 AGTGAAGATCAGATCCCGGTTGGTTTGTACAGATTTCTCTAGGAGACTAAAACATATTCAT 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGTGAAGATCAGATCCCGGTTGGTTTGTACAGATTTCTCTAGGAGACTAAAACATATTCAT 360

Qy   361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420

Qy   421 ATGGTGGCAAAGCTTGGGGGACTTGGTATAGCAAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGTGGCAAAGCTTGGGGGACTTGGTATAGCAAGCAAGAGTCCTGAATAATTCCATGGAACTT 480

Qy   481 GCTCGGAACTTGTATTGGAACACACCTTACTACCTTGTCCCCAGAGATCTGTCAGAATAAACCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCTCGGAACTTGTATTGGAACACACCTTACTACCTTGTCCCCAGAGATCTGTCAGAATAAACCC 540

Qy 541 TACAACAATAAAACGATATTGGTCTCTTGCTGTGTCTTATATGAGCTCTGCACACTT 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 TACAACAATAAAACGATATTGGTCTCTTGCTGTGTCTTATATGAGCTCTGCACACTT 600

Qy 601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAGATTGTCAAGCACAT 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAGATTGTCAAGCACAT 660

Qy 661 TTTGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTGATATCTCAGCTCTTT 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 TTTGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTGATATCTCAGCTCTTT 720

Qy 721 CAAGTATCTCCTCGAGACCGACCACCATCCATTAAATTCCATTTGAAAAGGCCCTTTTTAGAG 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 CAAGTATCTCCTCGAGACCGACCACCATCCATTAAATTCCATTTGAAAAGGCCCTTTTTAGAG 780

Qy 781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT 840

Qy 841 ATATGCAGAGCAGGAGCGCAGCTTCTCGGACATGCTGGGGAAGGTGGTCCAGAAGTGTA-A 899
        ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db 841 ATATGCAGAGCAGGAGCGCAGCTTCTCGGACATGCTGGGGAAGGTGGTCCAGAGGCATACT 900

Qy 900 AATACAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATCAAGGATATCTGTGCCAAT 959
        |||||||||||||||| ||||| |||||||||||||||||||||||||||||||||||
Db 901 GGTGTGAGGAGTGGGCTCTCAAGGCCTTGGCAGCTCCTGCTCCTGAGGCTTTGCAGGCTA 960

Qy 960 TAAAAGGAATGCTATATTGCATAGAAATGAATGAGAAAGACCACCACCCAGAGAGGC 1019
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 CAGCCCCTGCGGCTGCTGCTTCCACAGG---------------------------- 1007

Qy 1020 CAGATCTATAAAAATGATAGAAAGACCCCAAAATTGCTCGCTGCTGTGGACATTATGATTA 1079
        ---CTGCTGTTGAGTGTCTGTGGACATTATGATTA 1067
Db 1008 TTTCCAGATAAAAATGATAGAAAGACCCCAAAATTGCTCGCTGCTGTGGACATTATGATTA 1067

Qy 1080 TTATTATGTCAACTTGATATGCTGAGAGGAGAGCCCACAAACCAAGTTATCACCCTAT 1139
        |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db 1068 TTATTATGTCAACTTGATATGCTGAGAGGAGAGCCCACAAACCAAGTTATCACCCTAT 1127

Qy 1140 TCCTTCAAGAAAATACTCGAGTTGAGGATTACGGTCAGGAAAACACGAGGCATGGTCCATCCCC 1199
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1128 TCCTTCAAGAAAATACTCGAGTTGAGGATTACGGTCAGGAAAACACGAGGCATGGTCCATCCCC 1187

Qy 1200 AAGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAA 1259
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1188 AAGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAA 1247

Qy 1260 AGTGGAGAAGCAATGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACA 1319
        ||||||||||||||||||||----------------------------------
Db 1248 AGTGGAGAAGCAATT-- 1262

Qy 1320 AGAGCTAAGAGTAATGGGAGAGCCTAGATTCCAGGAGAGCTGCCATTAGGAAAAACGA 1379

Db 1263 -- 1262

Qy 1380 AATGAAGGAACAGAGAATATTGGAGCAGTTAGAGGAATACGGCCAACAGTACCAACAATGA 1439
        -------GGAATATTGGAGCAGTTAGAGGAAATACGGCCAACAGTACCAACAATGA 1310
Db 1263 --------GGAATATTGGAGCAGTTAGAGGAAATACGGCCAACAGTACCAACAATGA 1310

Qy 1440 CATGAAAGAAAATTAGCAAGAAGATGGGAGGAGAAGATGGGAGGAGAACCAGGA 1499
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1311 CATGAAAGAAAATTAGAAAGAAGATGGGAGGAGAAGAACCAG------------- 1348

Qy 1500 TAAAACCTATTGGTGAAGAAGACATTGAAGAACAAATGAGGCTTCAGAACACAAAGGA 1559

Db 1349 --- 1348

Qy 1560 AGCACCTGTGCAGGACATTGAAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGA 1619

Db 1349 ----------AGGACATTGAAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGA 1397

```
CC   the enzyme and effectively reduce its activity, as a bait protein in a
CC   two-hybrid or three-hybrid assay to identify other proteins which bind to
CC   or interact with the human NEK-like serine/threonine kinase polypeptide
CC   and modulate its activity, and for the immunisation of mammals. The
CC   current sequence represents human NEK-like serine/threonine protein
CC   kinase encoding DNA
XX
SQ   Sequence 1918 BP; 615 A; 367 C; 460 G; 476 T; 0 U; 0 Other;

     Query Match       66.3%;   Score 1359.8;   DB 8;   Length 1918;
     Best Local Similarity   84.5%;   Pred. No. 0;
     Matches 1673;   Conservative   0;   Mismatches   82;   Indels   224;   Gaps   4;

Qy       1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCCAAGGTGCCTTCGGGAAAGCATACTTA 60
           |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db      23 ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGCCAAGGTGCCTTCGGGAAAGCATACTTA 82

Qy      61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGATCAATTTTGAAAAGATG 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      83 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGATCAATTTTGAAAAGATG 142

Qy     121 CCCATACAAGAAAAAGAAGAGCTTCAAAGAAGAAGAAGTGATTCTTCTGGAAAGAGATGAAACAT 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     143 CCCATACAAGAAAAAGAAGAGCTTCAAAGAAGAAGAAGTGATTCTTCTGGAAAGAGATGAAACAT 202

Qy     181 CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGAGAATGGCAGGCTGTTATTGTAATG 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     203 CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGAGAATGGCAGGCTGTTATTGTAATG 262

Qy     241 GAATATTGTGATGGAGGGGATCTCATGAAAAAGGATCAATAGACAACGGGGTGTGTTATTT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     263 GAATATTGTGATGGAGGGGATCTCATGAAAAAGGATCAATAGACAACGGGGTGTGTTATTT 322

Qy     301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTACAGACATATTCATCAT 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     323 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTACAGACATATTCAT 382

Qy     361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     383 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 442

Qy     421 ATGGTGGCAAAGCTTGGGGACTTTGGTATAGCAAGACTTCCTGAATAATTCCATGGAACTT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     443 ATGGTGGCAAAGCTTGGGGACTTTGGTATAGCAAGACTTCCTGAATAATTCCATGGAACTT 502

Qy     481 GCTCGAACTTGTATTGGAACACCTTACTTCCGGGGTTTCTCCATTCCTTGATATCCAGCTCTT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     503 GCTCGAACTTGTATTGGAACACCTTACTTCCGGGGTTTCTCCATTCCTTGATATCTCAGCTCTT 562

Qy     541 TACAACAATAAAACGGATATTTGGTCTTCTTGGCTGTGTGTCTTATATGAGCTCTGCACACTT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     563 TACAACAATAAAACGGATATTTGGTCTTCTTGGCTGTGTGTCTTATATGAGCTCTGCACACTT 622

Qy     601 AACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTCAGAGATTTGTCAAGCACAT 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     623 AACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTCAGAGATTTGTCAAGCACAT 682

Qy     661 TTTGCCCAATATCTCCGGGGTTTTCTCGGAGCTCCATTCCTTGATATCTCAGCTCTT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     683 TTTGCCCAATATCTCCGGGGTTTTCTCGGAGCTCCATTCCTTGATATCTCAGCTCTT 742

Qy     721 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCATTTTGAAAAGGCCCTTTTTAGAG 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     743 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCATTTTGAAAAGGCCCTTTTTAGAG 802

Qy     781 AATCTTATTCCCAAATATTGACTCCGAGGTCATTCCGGAGAATTCAGTGCACATGCTT 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     803 AATCTTATTCCCAAATATTGACTCCGAGGTCATTCCGGAGAATTCAGTGCACATGCTT 862

Qy     841 ATATGCAGAGCAGGAGCGCCAGCTTCCGACATGCTGGGAAGTGGTTCCAGAAGTGTA-A 899
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     863 ATATGCAGAGCAGGAGCGCCAGCTTCCGACATGCTGGGAAGTGGTTCCAGAGGGCATACT 922
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Qy    1620 AAGTAAAAATCCAGAACACGAAATATAAAGCTAAGAGAAGGGGGTAAAAATTTGAAATTAATTT 1679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1398 AAGTAAAAATCCAGAACACGAAATATAAAGCTAAGAGAAGGGGGTAAAAATTTGAAATTAATTT 1457

Qy    1680 AGACAAATGTAATTCTGATGAAAAACATCTCCAGAGGAGGAGGAGCAATCGATATACCAAA 1739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1458 AGACAAATGTAATTCTGATGAAAAACATCTCCAGAGGAGGAGGAGGCAATGGATATACCAAA 1517

Qy    1740 TGAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATCAATGTGTAAAGGAGGCA 1799
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1518 TGAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGAATGTGTAAAGGAGGCA 1577

Qy    1800 TGGAGATTATACAGACAAAGCATTGAAAAACTTCACTGCCCAGAAGCAGGGTTTTCCAC 1859
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1578 TGGAGATTATACAGACAGACAAAGCATTGAAAAACTTCACTGCCCAGAAGCAGGGTTTTCCAC 1637

Qy    1860 GCAGACTGTAGCTCGTGTGGGAAACAGGAGGCAGTGGGATGGTGGGACCTCCACCTGCCCTCAGACTCT 1919
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1638 GCAGACTGTAGCTCGTGTGGGAAACAGGAGGCAGTGGGATGGTGGGAGCGCCTCCAGACTCT 1697

Qy    1920 GCTGCAGATGATGGCAGTGGCCGACATCACCTCCACCTGCCCACGGGGCCTGACAGTG 1978
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1698 GCTGCAGATGATGGCAGTGGCCGACATCACCTCCACCTGCCCACGGGGCCTGACAATG 1756
```

RESULT 8
AB259717
ID   AB259717 standard; DNA; 1918 BP.
XX
AC   AB259717;
XX
DT   17-APR-2003 (first entry)
XX
DE   Human NEK-like serine/threonine protein kinase DNA # SEQ ID 4.
XX
KW   Human; NEK-like serine/threonine protein kinase; cytostatic; cardiant;
KW   antiinflammatory; nootropic; neuroprotective; cancer; colon cancer;
KW   cardiovascular disorder; diabetes; COPD; CNS disorder; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003000903-A2.
XX
PD   03-JAN-2003.
XX
PF   24-JUN-2002; 2002WO-EP006948.
XX
PR   25-JUN-2001; 2001US-0300068P.
PR   07-DEC-2001; 2001US-0336704P.
XX
PA   (FARB) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; 2003-184051/18.
XX
PT   New polynucleotide encoding a NEK-like serine/threonine kinase
PT   polypeptide useful for treating diseaes associated with kinase
PT   dysfunction, e.g. cardiovascular disorders, cancer such as colon cancer,
PT   diabetes and CNS disorders.
XX
PS   Disclosure; Fig 4; 149pp; English.
XX
CC   The invention relates to a newly isolated polynucleotide encoding an NEK-
CC   like serine/threonine protein kinase. The activity of the polynucleotide
CC   and polypeptide of the invention may be described as cytostatic,
CC   cardiant, antiinflammatory, nootropic and neuroprotective. The expression
CC   vector and reagent of the invention are useful for the preparation of a
CC   medicament for modulating the activity of an NEK-like serine/threonine
CC   kinase in a disease, such as cancer (e.g. colon cancer), cardiovascular
CC   disorder, diabetes, COPD or CNS disorder. The polypeptides may also be
CC   used to identify compounds which may act as activators or inhibitors at
CC   the enzyme's active site, to raise specific antibodies which can block

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RESULT 9
ABX72263
ID   ABX72263 standard; cDNA; 1587 BP.
XX
AC   ABX72263;
XX
DT   03-JUN-2003  (first entry)
XX
DE   Human NOVX polynucleotide #94.
XX
KW   Human; NOVX; gene; ss; metabolic disorder; cardiomyopathy; diabetes; ASD;
KW   hypertension; congenital heart defect; aortic stenosis; valve disease;
KW   atrial septal defect; atrioventricular canal defect; ductus arteriosus;
KW   pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;
KW   tuberous sclerosis; scleroderma; atherosclerosis; infectious disease;
KW   obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;
KW   Parkinson's disease; immune disorder; haematopoietic disorder;
KW   haemophilia; hypercoagulation; Crohn's disease; cancer.
XX
OS   Homo sapiens.
XX
PN   WO20281498-A2.
XX
PD   17-OCT-2002.
XX
PF   03-APR-2002; 2002WO-US010780.
XX
PR   03-APR-2001; 2001US-0281086P.
PR   03-APR-2001; 2001US-0281136P.
PR   05-APR-2001; 2001US-0281863P.
PR   05-APR-2001; 2001US-0281906P.
PR   06-APR-2001; 2001US-0282020P.
PR   10-APR-2001; 2001US-0282930P.
PR   10-APR-2001; 2001US-0282934P.
PR   12-APR-2001; 2001US-0283512P.
PR   13-APR-2001; 2001US-0283710P.
PR   17-APR-2001; 2001US-0284234P.
PR   19-APR-2001; 2001US-0285325P.
PR   20-APR-2001; 2001US-0285381P.
PR   20-APR-2001; 2001US-0285609P.
PR   23-APR-2001; 2001US-0285748P.
PR   23-APR-2001; 2001US-0285890P.
PR   25-APR-2001; 2001US-0286068P.
PR   24-APR-2001; 2001US-0286292P.
PR   27-APR-2001; 2001US-0287213P.
PR   02-MAY-2001; 2001US-0288257P.
PR   29-MAY-2001; 2001US-0294164P.
PR   30-MAY-2001; 2001US-0294484P.
PR   18-JUN-2001; 2001US-0298952P.
PR   19-JUN-2001; 2001US-0299237P.
PR   19-JUN-2001; 2001US-0299276P.
PR   12-SEP-2001; 2001US-0318750P.
PR   25-SEP-2001; 2001US-0324802P.
PR   25-SEP-2001; 2001US-0325684P.
PR   27-SEP-2001; 2001US-0330143P.
PR   17-OCT-2001; 2001US-0332131P.
PR   14-NOV-2001; 2001US-0332240P.
PR   14-NOV-2001; 2001US-0332779P.
PR   21-NOV-2001; 2001US-0321115P.
PR   04-DEC-2001; 2001US-0337621P.
PR   03-JAN-2002; 2002US-0345783P.
PR   16-JAN-2002; 2002US-0350251P.
PR   02-APR-2002; 2002US-0011427O.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Guo X, Kekuda R,  Miller CE,  Malyankar UM,  Spytek KA;
PI   Patturajan M, Liu X,  Gusev VY,  Li L,  Vernet CAM, Zerhusen BD;
PI   Gorman L, Shenoy SG,  Pena CEA,  Smithson G,  Burgess CE,  Gerlach V;
PI   Padigaru M,  Shimkets RA, Gangolli EA, Taupier RJ,  Casman SJ,  Ji W;
PI   Anderson DW,  Leite MW, Rastelli L,  Edinger SR,  Stone DJ;
PI   Macdougall JR, Rothenberg ME, Mazur A, Millet I,  Peyman JA;
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Qy   900  AATACAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATCAAGGATATCTGTGCCAAT   959
                   |||||||||||||| |||||||  ||       |||||||||
Db   923  GGTGAGGAGTGGGCTTCTCAAGGCCTTGGCAGCTCTGCTCCTGAGGCCTTGCAGGCTA   982

Qy   960  TAAAAGGAATGCTATATTGCATAGAAATGATGGAGACACCAGCTCGGAGCCCAGAAGGC   1019
                                              |||||
Db   983  CAGCCCCTGCGGCGTGCTCTCACGG----------CTGCTGTTGAGTGTCTGCGGCT   1029

Qy   1020 CAGATCTATAAAAATGATAGAAAGACCCAAAATTGTGCTGCTGTGTGGACATTATGATTA   1079
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 TTTCCAGATAAAAATGATAGAAAGACCCAAAATTGCTGCTGTGTGGACATTATGATTA   1089

Qy   1080 TTATTATGTCTCAACTTGATATGCTGAGGAGGAGCCCACAAACCAAGTTATCACCCTAT   1139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1090 TTATTATGTCTCAACTTGATATGCTGAGGAGGAGCCCACAAACCAAGTTATCACCCTAT   1149

Qy   1140 TCCTCAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCATGGTCCATCCCC   1199
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1150 TCCTCAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCATGGTCCATCCCC   1209

Qy   1200 AAGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTGAAGCTCAACAATATAAGTTGAA   1259
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1210 AAGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTGAAGCTCAACAATATAAGTTGAA   1269

Qy   1260 AGTGGAGAAGCAATTGGGTCTTCGTCCCATCTTCTGCCGAGCCAAATTACAACCAGAGACA   1319
           |||||||||||||||
Db   1270 AGTGGAGAAGCAATT--------------------------------------------   1284

Qy   1320 AGAGCTAAGAAGTAATGGAGAGAGAGAGCCTAGATTCCAGGAGTCGCATTAGGAAAAAACGA   1379
                    |||||||||||||||||||||||||||||||||||||||||||
Db   1285 --------------GGAATATTGGAAGCAGTTAGAGGAAATACGGCCAACAGTACCACAATGA   1332

Qy   1380 AATGAAGGAACAGGAATATTGGAAGCAGTTAGAGGAAATACGGCCAACAGTACCACAATGA   1439
                                          |||||||||||||||||||||||||||||||
Db   1285 --------------GGAATATTGGAAGCAGTTAGAGGAAATACGGCCAACAGTACCACAATGA   1332

Qy   1440 CATGAAAGAAATTAGAGAAGAAGGATGGGGAGGAGAACCAGAGGAGAACTCAAAAATAAGTCA   1499
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1333 CATGAAAGAAATTAGAGAAGAAGGATGGGGAGGAGAACCAG------------------   1370

Qy   1500 TAAAACCTATTTGGTGAGGAGAGTAACCTGCCTGTCCATCAAGATGCATCTGAGGGAGA   1559
Db   1371 --------------------------------------------------------   1370

Qy   1560 AGACCTGTGCAGGACATTGAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGA   1619
                                        |||||||||||||||||||||
Db   1371 --------AGGACATTGAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGA   1419

Qy   1620 AAGTAAAAATCCAGAACAGAAGATATAAAGCTAAGAGGGGGTAAAATTTGAAATTAATTT   1679
                              ||||||||||||||||||||||||||||||||||||||
Db   1420 AAGTAAAAATCCAGAACAGAAGATATAAAGCTAAGAGGGGGTAAAATTTGAAATTAATTT   1479

Qy   1680 AGACAAATGTATTTCTGATGAAAACATCCTCCAAGAGGCAATGAGGCAATGGATATACCAAA   1739
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 AGACAAATGTATTTCTGATGAAAACATCCTCCAAGAGGCAATGAGGCAATGGATATACCAAA   1539

Qy   1740 TGAAACTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGTGTAAAGGAGCA   1799
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TGAAACTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGTGTAAAGGAGCA   1599

Qy   1800 TGGAGATTATACAGACAAAGCATTTGAAAAACTTCACTGCCCAGAGAGCAGGGTTTTCCAC   1859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 TGGAGATTATACAGACAAAGCATTTGAAAAACTTCACTGCCCAGAGAGCAGGGTTTTCCAC   1659

Qy   1860 GCAGACTGTAGCTGCTGTGGGAAACAGGAGCAGTGGGATGGAGGAGCGCCTCAGACTCT   1919
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 GCAGACTGTAGCTGCTGTGGGAAACAGGAGCAGTGGGATGGAGGAGCGCCTCAGACTCT   1719

Qy   1920 GCTGCAGATGATGGCAGTGGCCAGCATCACCTCCACCTGCCCCACCTGCGCCCACGGGGCCTGACAGTG   1978
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 GCTGCAGATGATGGCAGTGGCCGCCGCCACATCACCTCCACCTGCCCCACCTGCGCCCGGGGCCTGACAATG   1778
```

PI Ellerman K;
XX
DR WPI; 2003-046858/04.
DR P-PSDB; ABU54635.
XX
PT New isolated NOVX polypeptide useful for treating atherosclerosis,
PT metabolic disorders, diabetes, obesity, infectious disease, anorexia,
PT neurodegenerative disorders, Alzheimer's disease and cancer.
XX
PS Claim 17; Page 291-292; 666pp; English.
XX
CC The invention relates to human polypeptides, termed NOVX, and the
CC polynucleotides encoding them. The polypeptides and polynucleotides are
CC useful for diagnosing disease, and screening for potential therapeutic
CC agents. The sequences are useful for treating metabolic disorders,
CC cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic
CC stenosis, atrial septal defect (ASD), atrioventricular canal defect,
CC ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
CC septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma,
CC atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
CC and cancer. Sequences ABX72170-ABX72275 represent human NOVX
CC polynucleotides of the invention
XX
SQ Sequence 1587 BP; 513 A; 313 C; 347 G; 414 T; 0 U; 0 Other;

Query Match   58.0%;   Score 1190.2;   DB 8;   Length 1587;
Best Local Similarity 99.5%;   Pred. No. 0;
Matches 1205;   Conservative 0;   Mismatches 3;   Indels 3;   Gaps 1;

Qy   1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAAGCATACTTA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   99 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAAGCATACTTA 158

Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATGAATCAATTTTGAAAAGAGATG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   159 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGAGATG 218

Qy   121 CCCATACAAGAAAAAGAAGCTTCAAGAAGAAGTGATTCTTCTGGAAAAGATGAAACAT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   219 CCCATACAAGAAAAAGAAGCTTCAAGAAGAAGTGATTCTTCTGGAAAAGATGAAACAT 278

Qy   181 CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAGAATGGCAGGCTGTGTTATTGTAATG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   279 CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAGAATGGCAGGCTGTTTATTGTAATG 338

Qy   241 GAATATTGTGATGGAGGGGATCTCATGAAAAAGATCAATAGACAACGGGGTGTGTTATTT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   339 GAATATTGTGATGGAGGGGATCTCATGAAAAAGATCAATAGACAACGGGGTGTGTTATTT 398

Qy   301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGAGATTTCTCTAGGACTAAAACATATTCAT 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   399 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGAGATTTCTCTAGGACTAAAACATATTCAT 458

Qy   361 GACAGGAAGAGATATTACACAGGAGCATAAAAGTTCAGAAGACATTTTCTTAGCAAGAACGGA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   459 GACAGGAAGAGATATTACACAGGAGCATAAAAGTTCAGAAGACATTTTCTTAGCAAGAACGGA 518

Qy   421 ATGGTGGCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGGACTT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   519 ATGGTGGCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAGTTCCATGGGACTT 578

Qy   481 GCTCGAACTTGTATTGGAACACACCTTACACCTGTCCCCAGATCGTCGTCCCCAGAATAAACCC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   579 GCTCGAACTTGTATTGGAACACCTTACACCTGTCCCCAGATCGTCGTCCCCAGAATAAACCC 638

Qy   541 TACAACAATAAAACGGATATTGGTCTTCTTGGCTGTCTCTTATATGAGCTCTGCACACTT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   639 TACAACAATAAAACGGATATTTGGTCTTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT 698

Qy   601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTACGCAGCAGCTGGTTCTGCAAGCACAT 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   699 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTACGCAGCAGCTGGTTCTGCAAGCACAT 758

Qy   661 TTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   759 TTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 818

Qy   721 CAAGTATCTCCTCGAGACCGACCATCATAAATTCCATTTGAAAAGCCCTTTTTTAGAG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   819 CAAGTATCTCCTCGAGACCGACCATCCATCCATTCCATTTGAAAAGCCCTTTTTTAGAG 878

Qy   781 AATCTTATTCCCAAATATTGACTCCTGAGGTCA---TTCAGGAAGAATTCAGTCACATG 837
           |||||||||||||||||||||||||| ||
Db   879 AATCTTATTCCCAAATATTTGACTCCTGAGGTCAGTTTGAGGAAGAATTCAGTCACATG 938

Qy   838 CTTATATGCAGAGCAGGAGCGCCAGCTTCTCGACATGCTGGGAAGGTGGTCCAGAAGTGT 897
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   939 CTTATATGCAGAGCAGGAGCGCCAGCTTCTCGACATGCTGGGAAGGTGGTCCAGAAGTGT 998

Qy   898 AAAATACAAAAAGTGAGATTCCAGGGAAGTGCCCACCAAGATCAAGGAGATATCGTGTGCCA 957
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   999 AAAATACAAAAAGTGAGATTCCAGGGAAGTGCCCACCAAGATCAAGGAGATATCGTGCCA 1058

Qy   958 ATTAAAAGGAATGCTATATTGCATAGAAAATGAATGGAAATGAATGGACACCAAATTGCTG 1017
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1059 ATTAAAAGGAATGCTATATTGCATAGAAAATGAATGGAAATGAATGGACACCAAATTGCTG 1118

Qy   1018 GCCAGATCTATAAAAATGATAGAAAGACCAAATTGCTGTCTGTCTGTGGACATTATGAT 1077
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1119 GCCAGATCTATAAAAATGATAGAAAGACCAAATTGCTGTCTGTCTGTGGACATTATGAT 1178

Qy   1078 TATTATTATGCTCAACTGATATGCTGAGGTGAGGATTACGGTCAGGAAACCAAGTTATCACCCT 1137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1179 TATTATTATGCTCAACTGATATGCTGAGGTGAGGATTACGGTCAGGAAACCAAGTTATCACCCC 1238

Qy   1138 ATTCCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCATGGTCCATCC 1197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1239 ATTCCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCATGGTCCATCC 1298

Qy   1198 CCAAGTCAATG 1208
           |||||||||||
Db   1299 CCAAGTCAATG 1309

RESULT 10
ABX72262
ID ABX72262 standard; cDNA; 1453 BP.
XX
AC ABX72262;
XX
DT 03-JUN-2003 (first entry)
XX
DE Human NOVX polynucleotide #93.
XX
KW Human; NOVX; gene; ss; metabolic disorder; cardiomyopathy; diabetes; ASD;
KW hypertension; congenital heart defect; aortic stenosis; valve disease;
KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
KW pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;
KW tuberous sclerosis; scleroderma; atherosclerosis; infectious disease;
KW obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;
KW Parkinson's disease; immune disorder; haematopoietic disorder;
KW haemophilia; hypercoagulation; Crohn's disease; cancer.
XX
OS Homo sapiens.
XX
PN WO200281498-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010780.
XX
PR 03-APR-2001; 2001US-0281086P.
PR 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.

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PR  05-APR-2001;  2001US-0281906P.
PR  06-APR-2001;  2001US-0282020P.
PR  10-APR-2001;  2001US-0282930P.
PR  10-APR-2001;  2001US-0282934P.
PR  12-APR-2001;  2001US-0283512P.
PR  13-APR-2001;  2001US-0283710P.
PR  17-APR-2001;  2001US-0284234P.
PR  19-APR-2001;  2001US-0285325P.
PR  20-APR-2001;  2001US-0285381P.
PR  20-APR-2001;  2001US-0285509P.
PR  23-APR-2001;  2001US-0285748P.
PR  23-APR-2001;  2001US-0285890P.
PR  24-APR-2001;  2001US-0286068P.
PR  25-APR-2001;  2001US-0286292P.
PR  27-APR-2001;  2001US-0287213P.
PR  02-MAY-2001;  2001US-0288257P.
PR  29-MAY-2001;  2001US-0294164P.
PR  30-MAY-2001;  2001US-0294484P.
PR  18-JUN-2001;  2001US-0298952P.
PR  19-JUN-2001;  2001US-0299237P.
PR  19-JUN-2001;  2001US-0299276P.
PR  12-SEP-2001;  2001US-0318750P.
PR  25-SEP-2001;  2001US-0324800P.
PR  25-SEP-2001;  2001US-0324802P.
PR  27-SEP-2001;  2001US-0325684P.
PR  17-OCT-2001;  2001US-0330143P.
PR  14-NOV-2001;  2001US-0332131P.
PR  14-NOV-2001;  2001US-0332240P.
PR  14-NOV-2001;  2001US-0332779P.
PR  21-NOV-2001;  2001US-0332115P.
PR  04-DEC-2001;  2001US-0337621P.
PR  03-JAN-2002;  2002US-0345783P.
PR  16-JAN-2002;  2002US-0350251P.
PR  02-APR-2002;  2002US-0114270.
XX
PA  (CURA-) CURAGEN CORP.
XX
PI  Guo X, Kekuda R, Miller CB, Malyankar UM, Spytek KA;
PI  Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD;
PI  Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Gerlach V;
PI  Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ, Ji W;
PI  Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
PI  Macdougall JR, Rotherberg ME, Mazur A, Millet I, Peyman JA;
PI  Ellerman K;
XX
DR  WPI; 2003-046858/04.
DR  P-PSDB; ABU54634.
XX
PT  New isolated NOVX polypeptide useful for treating atherosclerosis,
PT  metabolic disorders, diabetes, obesity, infectious disease, anorexia,
PT  neurodegenerative disorders, Alzheimer's disease and cancer.
XX
PS  Claim 17; Page 291; 666pp; English.
XX
CC  The invention relates to human polypeptides, termed NOVX, and the
CC  polynucleotides encoding them. The polypeptides and polynucleotides are
CC  useful for diagnosing disease, and screening for potential therapeutic
CC  agents. The sequences are useful for treating metabolic disorders,
CC  cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic
CC  stenosis, atrial septal defect (ASD), atrioventricular canal defect,
CC  ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
CC  septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma,
CC  atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
CC  disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
CC  haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
CC  and cancer. Sequences ABX72170-ABX72275 represent human NOVX
CC  polynucleotides of the invention
XX
SQ  Sequence 1453 BP; 466 A; 283 C; 309 G; 395 T; 0 U; 0 Other;

Query Match             57.4%;  Score 1178.4;  DB 8;  Length 1453;
Best Local Similarity   99.2%;
Matches 1198;  Mismatches    0;  Conservative    0;  Indels    1;  Gaps    1;
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```
Qy     1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCAAGTGCCTTCGGGAAGAAGCATACTTA  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCAAGTGCCTTCGGGAAGAAGCATACTTA  60

Qy    61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGATG 120
         |||||||||||||||||||||||||||||| ||||||| |||||||||||||||||
Db    61 GCTAAAGGGAAATCAGATAGCAAGCACTGT-CATAAAAG-GATCAATTTTGAAAAG---  117

Qy   121 CCCATACAAGAAAAGAGAGCTTCAAGAAGAAGTGATTCTTCTGGAAAAGATGAAACAT  180
         ||||||||||||||||||||||||||||||||||||||||||
Db   118 ------CAAGAAAAAGAGAGCTTCAAGAAGAAGTGATTCTTCTGGAAAAAGAGATGAAACAT  171

Qy   181 CCCAACATTGTAGCCTTCAATTCATTCAAGAGAATGGCAGGCGTGTTATTGTAATG  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   172 CCCAACATTGTAGCCTTCAATTCATTCAAGAGAATGGCAGGCGTGTTATTGTAATG  231

Qy   241 GAATATTGTGATGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATTT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   232 GAATATTGTGATGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATTT  291

Qy   301 AGTGAAGATCAGATCCTCGGTTGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   292 AGTGAAGATCAGATCCTCGGTTGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT  351

Qy   361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACCGA  420
         |||| |||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   352 GACACGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA  411

Qy   421 ATGGTGGCAAAGCTCTGGGGACTTTGGTATAGCAGTCCTGAATAATTCCATGGAACTT  480
         ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   412 ATGGTGGCAAAGCTTGGGGACTTTGGTATAGCAGTCCTGAATAATTCCATGGAACTT  471

Qy   481 GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCGTCAGAATAAACCC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   472 GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCGTCAGAATAAACCC 531

Qy   541 TACAACAATAAAAGGGGATATTTGGTCTCTTGGCGTGTCTTATGAGCTCGCACACTT  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   532 TACAACAATAAAAGGGGATATTTGGTCTCTTGGCGTGTCTTATGAGCTCGCACACTT  591

Qy   601 AAACATCCTTTGAGGTAACAACTTACAGCAGCTGGTCTGAAGATTTGTCAAGCACAT  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   592 AAACATCCTTTGAGGTAACAACTTACAGCAGCTGGTCTGAAGATTTGTCAAGCACAT  651

Qy   661 TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   652 TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 711

Qy   721 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTAGAG 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   712 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTAGAG 771

Qy   781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGGAATTCAGTCACATGCTT 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   772 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGGAATTCAGTCACATGCTT 831

Qy   841 ATATGCAGAGCAGGAGCGCGCAGCTTCTCGACATGCTGGGAAGGTGGTCCAGAAGTGTAA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   832 ATATGCAGAGCAGGAGCGCGCAGCTTCTCGACATGCTGGGAAGGTGGTCCAGAAGTGTAA 891

Qy   901 ATACAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATCTCAAGGATATCTGTGCCAATT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   892 ATACAAAAGTGAGATTCCAGGGAAAGTGCCCACCAAGATCTCAAGGATATCTGTGCCAATT 951

Qy   961 AAAAGGAATGCTATATTGCATAGAAATGATAGAAAGACCCAAAATTGCTGTGGACCAGAAGGCC 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   952 AAAAGGAATGCTATATTGCATAGAAATGATAGAAAGACCCAAAATTGCTGTGGACCAGAAGGCC 1011

Qy  1021 AGATCTATAAAAATGATAGAAAGACCCAAAATTGCTGTCTGTGGACATTATGATTAT 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1012 AGATCTATAAAAATGATAGAAAGACCCAAAATTGCTGTCTGTGGACATTATGATTAT 1071
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CC          disorders (e.g. allograft rejection or graft vs. host disease), cancers
CC          (e.g. leukaemias) or wound granulation
XX
SQ          Sequence 1632 BP; 459 A; 354 C; 415 G; 404 T; 0 U; 0 Other;

Query Match             29.3%;  Score 602;  DB 10;  Length 1632;
Best Local Similarity   98.4%;  Pred. No. 6.3e-154;
Matches   608;  Conservative   0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy        204 TTCATTTCAAGAGAATGGCAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGGATCT 263
              ||| || ||||||||||||||||||| || |||||||| |||||||||||||||||||||
Db        201 TTTTCTTACGAGAGAATGGCAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGGATCT 260

Qy        264 CATGAAAAGGATCAATAGACAACGGGGTGTGTTATTAGTGAGATCAGATCCTCGGTTG 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CATGAAAAGGATCAATAGACAACGGGGTGTGTTATTAGTGAAGATCAGATCCTCGGTTG 320

Qy        324 GTTTGTACAGATTTCTCTAGGACTAAAACATATTCATGACAGAAGAGATATTACCACAGGA 383
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTTTGTACAGATTTCTCTAGGACTAAAACATATTCATGACAGAAGAGATATTACCACAGGGA 380

Qy        384 CATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGAATGGTCGCAAAGCTTGGGGACTT 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 CATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGAATGGTCGCAAAGCTTGGGGACTT 440

Qy        444 TGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTTGCTCGAACTTGTATTGGAACACC 503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTTGCTCGAACTTGTATTGGAACACC 500

Qy        504 TTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCCTACAACAATAAAACGGATATTTG 563
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCCTACAACAATAAAACGGATATTTG 560

Qy        564 GTCTCTTGGCTGTCGTGTCTTATATGAGCTCTGCACACTTAAACATCCTTTTGAGGGTAACAA 623
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GTCTCTTGGCTGTCGTGTCTTATATGAGCTCTGCACACTTAAACATCCTTTTGAGGGTAACAA 620

Qy        624 CTTACAGCAGCTGGTTCTCGAAGATTGTCAAGCACATTTTGCCCCAATATCTCCGGGGTT 683
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 CTTACAGCAGCTGGTTCTCGAAGATTGTCAAGCACATTTTGCCCCAATATCTCCGGGGTT 680

Qy        684 TTCTCGTGAGCTCCATTCCTGATATCCTCAGCTCTTTTGAAAAGGCCCTTTTATTCCCAAATATTTGAC 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 TTCTCGTGAGCTCCATTCCTGATATCCTCAGCTCTTTTGAAAAGGCCCTTTTATTCCCAAATATTTGAC 740

Qy        744 ATCCATAAATTCCATTTTGAAAAGGCCCTTTTTATTCCCAAATATTTGAC 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 ATCCATAAATTCCATTTTGAAAAGGCCCTTTTTATTCCCAAATATTTGAC 800

Qy        804 TCCTGAGTCATTCAGGA 821
              |||||||||||||||||
Db        801 TCCTGAGTCGTAAGTTTTGA 818
```

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RESULT 12
ADF44502
ID   ADF44502 standard; cDNA; 1434 BP.
XX
AC   ADF44502;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Mouse kinase protein encoding cDNA SEQ ID NO:20.
XX
KW   cytostatic; nootropic; neuroprotective; antidiabetic; screening;
KW   regulation; drug development; protein-associated disease; cancer;
KW   dementia; diabetes; kinase; enzyme; mouse; gene; ss.
XX
OS   Mus musculus.
XX
PN   WO200308492-A1.
XX
PD   16-OCT-2003.
```

```
Qy       1081 TATTATGCTCAACTTGATATGCTGAGGAGGAGAGCCCACAAACCAAGTTATCACCCTATT 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 TATTATGCTCAACTTGATATGCTGAGGAGGAGAGCCCACAAAACCAAGTTATCACCCCATT 1131

Qy       1141 CCTCAAGAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAAACGAGGCATGGTCCATCCCCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 CCTCAAGAGAAAATACTGGGAGTTGGAGGATTACGGTCAGGAAAACGAGGCATGGTCCATCCCCA 1191

Qy       1201 AGTCAATG 1208
              ||||||||
Db       1192 AGTCAATG 1199
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RESULT 11
AB277151
ID   AB277151 standard; cDNA; 1632 BP.
XX
AC   AB277151;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human protein kinase encoding cDNA SEQ ID NO:51.
XX
KW   Human; protein kinase; enzyme; antiasthmatic; antiinflammatory;
KW   antidiabetic; antiparkinsonian; antimigraine; cardiant; cytostatic;
KW   immunosuppressive; vulnerary; gene therapy; COPD; asthma; migraine;
KW   chronic obstructive pulmonary disease; non-insulin dependent diabetes;
KW   Parkinson's disease; myocardial infarction; inflammatory bowel disease;
KW   autoimmune disorder; allograft rejection; graft versus host disease;
KW   cancer; leukaemia; wound granulation; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..1632
FT                  /tag= a
FT                  /partial
FT                  /product= "protein kinase"
FT                  /note= "no start or stop codons given"
XX
PN   WO2003000901-A2.
XX
PD   03-JAN-2003.
XX
PF   24-JUN-2002; 2002WO-IB002358.
XX
PR   26-JUN-2001; 2001US-0301098P.
PR   06-NOV-2001; 2001US-0332870P.
XX
PA   (DECO-) DECODE GENETICS EHF.
XX
PI   Martinez RAM, Sigurdsson GT;
XX
DR   WPI; 2003-201429/19.
DR   P-PSDB; ABP96073.
XX
PT   New protein kinase genes and polypeptides, useful for diagnosing diseases
PT   associated with a protein kinase, or in gene therapy for treating e.g.
PT   Parkinson's disease, migraine, myocardial infarction, allograft rejection
PT   or cancers.
XX
PS   Claim 1; Page 76; 258pp; English.
XX
CC   AB277126 to AB277165 encode the human protein kinases given in ABP96048
CC   to ABP96087. The protein kinases have antiasthmatic, antiinflammatory,
CC   antidiabetic, antiparkinsonian, antimigraine, cardiant, cytostatic,
CC   immunosuppressive and vulnerary activities, and can be used in gene
CC   therapy. A protein kinase therapeutic agent from the present invention,
CC   particularly a protein kinase gene agonist or antagonist, can be used for
CC   treating a disease or condition associated with a protein kinase in an
CC   individual. These diseases include chronic obstructive pulmonary diseases
CC   (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease,
CC   migraine, myocardial infarction, inflammatory bowel disease, autoimmune
```

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Db  221  --------GAAAAAGAGGCCTCAAAGAACGAGTGATTCTTCTGGCTAGGATGGAGCAT  271
              |||||||||||||||||||||||||||||||||||||||||||
Qy  181  CCCACATTGTAGCCTTCTCAATTCATTTCAGAGAGAATGGCAGGCTGTTTATTGTAATG  240

Db  272  CCCATATCGTAACCTTCTTCAGCTCGTTCAGAGAGAACGGCAGGCTGTTTATTGTAATG  331
              ||||||||||||||||||||||||||||||||||||||||||||
Qy  241  GAATATTGTGATGGAGGGGATCTCATGAAAAGATCAATAGACAACGGGGTGTGTTATTT  300

Db  332  GAATACTGTGATGGAGGGGATCTCATGCAGAGGCAGCCAGGACTAAAACATATTCAT    391
              |||||||||||||||||||||||||||||||||||||||||||
Qy  301  AGTGAAGATCAGATCCTCGGTTGGTTTGTTGTACAGATTTCCTAGGACTAAAACATATTCAT  360

Db  392  AGCGAAGACCAGATCCTGTTGTTGTTTGTTACAGATTTCCTAGGACTAAGCATATTCAT  451
              |||||||||||||||||||||||||||||||||||||||||||
Qy  361  GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA  420

Db  452  GACAGGAAGAGTTTTACACAGGGACATAAAAAATCTCAGAATATTTTCTTAGCAAGAATGA  511
              |||||||||||||||||||||||||||||||||||||||||||
Qy  421  ATGGTGGCAAAGCTTGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480

Db  512  ATGGTTGCCAAGCTCGGGGACTTTGGACAGCAAGAACACTGAATGACTCCATGGAACTT  571
              |||||||||||||||||||||||||||||||||||||||||||
Qy  481  GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCC  540

Db  572  GCTCAAACATGTGCTGGGACACCTTACTACCTGTCCCCAGAGAGATCTGTCAGAACAGGCCA  631
              |||||||||||||||||||||||||||||||||||||||||||
Qy  541  TACAACAATAAAAGCGGATATTTGGTCCTCTTGGCGTGTCTTTATATGAGCTCTGCACACTT  600

Db  632  TACAACAATAAAACGGACATCTGGTCTCTTGGCGTCTCTTGGCGTGTCTTATATGAGCTCTGCACACTC  691
              |||||||||||||||||||||||||||||||||||||||||||
Qy  601  AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAGCACAT  660

Db  692  AAGCATCCTTTTGAGGAGCAACAACTTCACCATCTGGTTCTGAAGATTTGTCAAGGACGT  751
              |||||||||||||||||||||||||||||||||||||||||||
Qy  661  TTTGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATANTCTCAGCTCTTT  720

Db  752  GTTGCTCCCATATCACCCCACTTCCTTCGTGACCTACAGTCCTTGATACCTCAGCTCTTC  811
              |||||||||||||||||||||||||||||||||||||||||||
Qy  721  CAAGTATCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTAGAG  780

Db  812  AGAGTGTCTCCTCCAGGACCGGCCATCCGTTACGTCCCTTTGAAAAGACCCTTTTTAGAA  871
              |||||||||||||||||||||||||||||||||||||||||||
Qy  781  AATCTTATTCCCAAATATTTGACTCCTGAGGTC-ATTCAGGAAGAATTCAGTCACATGCT  839

Db  872  ACTCTCATTGCCCGATCCTTGTATCCTGAGGTCTTGTTCAAGAAGAAGAATCCAGTCCCACGCT  931
              |||||||||||||||||||||||||||||||||||||||||||
Qy  840  TATATGCAGCAGCAGGAGCGCCAGCTTCTGCACATGCTGGGAAGTGGTCCAGAAGTGTAA  899

Db  932  CACATGGAGAACATGGCCATTGGCCCCACCAGCTGTGTTGGGAGAGTTAGTCCATGGTGGGAT  991
              |||||||||||||||||||||||||||||||||||||||||||
Qy  900  AATACAA  906
         ||   ||
Db  992  CATGTAA  998
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XX
PF   04-APR-2003; 2003WO-JP004330.
XX
PR   05-APR-2002; 2002JP-00103396.
PR   23-APR-2002; 2002JP-00129084.
PR   02-MAY-2002; 2002JP-00130601.
PR   04-DEC-2002; 2002JP-00352520.
XX
PA   (RIKE ) RIKEN KK.
PA   (DNAF-) DNAFORM KK.
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
PI   Hayashizaki Y,  Kamiya M,  Kubodera H,  Watanabe W;
XX
DR   WPI; 2003-833568/77.
DR   P-PSDB; ADF44528.
XX
PT   Proteins and encoded DNAs with kinase activity, useful in screening
PT   substances for regulating such activity and in developing drugs for the
PT   protein-associated diseases e.g. cancer, dementia and diabetes.
XX
PS   Claim 4; SEQ ID NO 20; 342pp; Japanese.
XX
CC   The present invention describes a protein: (a) containing any of the
CC   amino acid sequences of ADF44509 to ADF44534 or ADF44544; or (b) based on
CC   any of the sequences in (a) but with some amino acids deleted,
CC   substituted and/or added and having kinase activity. Also described: (1)
CC   a DNA encoding any of the proteins; (2) a full-length cDNA encoding the
CC   protein; (3) a DNA which is: (a) a DNA containing any of the base
CC   sequences in ADF44483 to ADF44508 or ADF44543; (b) a DNA derived from any
CC   of the sequences in (a) but with some bases deleted, substituted and/or
CC   added and encoding a protein with kinase activity; or (c) a DNA
CC   hybridisable with any of the sequences in (a) or their complementary
CC   strands under stringent conditions and encoding a protein with kinase
CC   activity; (4) a recombinant vector containing the DNA; (5) a cell
CC   transferred with the DNA or recombinant vector, or an individual produced
CC   from the cell; (6) recombinant proteins produced by such cells; (7) an
CC   oligonucleotide containing 5-10 consecutive bases in any of the base
CC   sequences, its sense oligonucleotide, an antisense oligonucleotide with a
CC   complementary strand of such sense oligonucleotide, or an oligonucleotide
CC   derivative of the (anti-)sense oligonucleotide; (8) an antibody
CC   specifically binding to the protein, or its partial fragment; (9) a
CC   method for screening substances for regulating activity of the protein by
CC   contacting a test substance with such protein before measuring changes in
CC   the protein activity due to the test substance; (10) a method for
CC   screening substances regulating expression of the DNA by contacting a
CC   test substance with cells transferred with the gene and detecting changes
CC   in expression level of the DNA in such cells; (11) recordable media for
CC   reading in a computer with information on the amino acid sequences of the
CC   proteins, and/or base sequences of the DNAs stored; and (12) a support
CC   for binding with any of the proteins and/or DNAs. The proteins and their
CC   encoded DNAs have cytostatic, nootropic, neuroprotective and antidiabetic
CC   activities. They can be used in screening substances for regulating such
CC   activity and in developing drugs for the protein-associated diseases e.g.
CC   cancer, dementia and diabetes. The present sequence is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 1434 BP; 392 A; 338 C; 336 G; 368 T; 0 U; 0 Other;

Query Match             29.0%;  Score 595.4;  DB 10;  Length 1434;
Best Local Similarity   80.3%;  Pred. No. 3.8e-152;
Matches  728;  Conservative    0;  Mismatches  166;  Indels  13;  Gaps    2;

Qy     1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCAAGGTGCCTTCGGGAAAGCATACTTA  60
         |||||||||||| |||||||| |||||  || |||||  ||||||||||  |||||  ||
Db   104 ATGGATAACTTCACCTGATTAAGATCATTGGGGAAGGCACCTTTGGGAAGGTGTACTTG 163

Qy    61 GCTAAAAGGGAAATCAGATAGAGCAAGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG 120
         ||||  ||||  ||||||     ||||||||| |  ||||||   ||||||| |||||||
Db   164 GCTAAAGATAAATCAGAAAGCAGTCACTCACTGTGTCATAAAAGAAATCAGTTTGACAAAG-- 220

Qy   121 CCCATACAAGAAGAAGAGAGCTTCAAAGAAGAAGAAGTGATTCTTCTGGAAAAGATGAAACAT 180
         |||||| |||  ||  |||| |  |||  |||| |  || |||| ||| | |||| | ||||
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PD   16-OCT-2003.
XX
PF   04-APR-2003; 2003WO-JP004330.
XX
PR   05-APR-2002; 2002JP-00103396.
PR   23-APR-2002; 2002JP-00120904.
PR   02-MAY-2002; 2002JP-00110601.
PR   04-DEC-2002; 2002JP-00352520.
XX
PA   (RIKE ) RIKEN KK.
PA   (DNAF-) DNAFORM KK.
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
PI   Hayashizaki Y, Kamiya M, Kubodera H, Watanabe W;
XX
DR   WPI; 2003-833568/77.
DR   P-PSDB; ADF44515.
XX
PT   Proteins and encoded DNAs with kinase activity, useful in screening
PT   substances for regulating such activity and in developing drugs for the
PT   protein-associated diseases e.g. cancer, dementia and diabetes.
XX
PS   Claim 4; SEQ ID NO 7; 342pp; Japanese.
XX
CC   The present invention describes a protein: (a) containing any of the
CC   amino acid sequences of ADF44509 to ADF44534 or ADF44544; or (b) based on
CC   any of the sequences in (a) but with some amino acids deleted,
CC   substituted and/or added and having kinase activity. Also described: (1)
CC   a DNA encoding any of the proteins; (2) a full-length cDNA encoding the
CC   protein; (3) a DNA which is: (a) a DNA containing any of the base
CC   sequences in ADF44483 to ADF44508 or ADF44543; (b) a DNA derived from any
CC   of the sequences in (a) but with some bases deleted, substituted and/or
CC   added and encoding a protein with kinase activity; or (c) a DNA
CC   hybridisable with any of the sequences in (a) or their complementary
CC   strands under stringent conditions and encoding a protein with kinase
CC   activity; (4) a recombinant vector containing the DNA; (5) a cell
CC   transferred with the DNA or recombinant vector, or an individual produced
CC   from the cell; (6) recombinant proteins produced by such cells; (7) an
CC   oligonucleotide containing 5-10 consecutive bases in any of the base
CC   sequences, its sense oligonucleotide, an antisense oligonucleotide with a
CC   complementary strand of such sense oligonucleotide, or an oligonucleotide
CC   derivative of the (anti-)sense oligonucleotide; (8) an antibody
CC   specifically binding to the protein, or its partial fragment; (9) a
CC   method for screening substances for regulating activity of the protein by
CC   contacting a test substance with such protein before measuring changes in
CC   the protein activity due to the test substance; (10) a method for
CC   screening substances regulating expression of the DNA by contacting a
CC   test substance with cells transferred with the gene and detecting changes
CC   in expression level of the DNA in such cells; (11) recordable media for
CC   reading in a computer with information on the amino acid sequences of the
CC   proteins, and/or base sequences of the DNAs stored; and (12) a support
CC   for binding with any of the proteins and/or DNAs. The proteins and their
CC   encoded DNAs have cytostatic, nootropic, neuroprotective and antidiabetic
CC   activities. They can be used in screening substances for regulating such
CC   activity and in developing drugs for the protein-associated diseases e.g.
CC   cancer, dementia and diabetes. The present sequence is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 2407 BP; 718 A; 528 C; 604 G; 557 T; 0 U; 0 Other;

Query Match     29.0%;  Score 595.4;  DB 10;  Length 2407;
Best Local Similarity  81.0%;  Pred. No. 5e-152;
Matches 722;  Conservative   0;  Mismatches 156;  Indels  13;  Gaps     2;

Qy        1 ATGGATAAGTACAGATGTGATTAAGGCCATCGGCGCCAAGGTGCCTCGGCGAAAGCCTATCAGTGTGCTTATTATGTTGTATGGTTTTGGGGTACTTA  60
            |||||||||||| |||| ||  ||||||||||||||| ||||| | ||||| |||||||||
Db       92 ATGGATAACTTTCACCTGATTAAGATCATTGGGGAAGGCACCTTTGGGAAGGCACGTGTACTTG 151

Qy       61 GCTAAAGGGAAATCAGATAGCAAGCAACTGTGTCATAAAGAGATCAATTTGAAAAGATG 120
            |||||| ||| | |||| |||| |||||| ||||| |||||||||||
Db      152 GCTAAAGATAAATCAGAAGCAGTCACTGTGTCATAAAGAGAAATCAGTTTGACAAAG--- 208

Qy      121 CCCATACACAGAAAAAAGAGAGCTTCAAGAAGAAGAGAGTGATTCTTCTGGAAAAGATGAAACAT 180
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Db      209 --------GAAAAGAGAGCCTCAAAGAACGAAGTGATTCTTCTGGCTAGGATGGATGGAGCAT 259
            |||||||| ||  | ||||  ||  |||||||||||||||||||| ||| |||
Qy      181 CCCAACATGTAGCTCTTCATTCATTCAAGATCATTCAGAGAAGAATGGCAGGCTGTTTATTGTAATG 240
            ||||| ||| || |||||||| |||| |||| ||||||||| |||| ||||| |||||| |||||
Db      260 CCCAATATCGTAACCTTCTTCAGCTGTTCAAGAGAACGGCAGGCTGTTTATTGTAATG 319
Qy      241 GAATATTGTGATGGAGGGGATCTCATGAAAAGGATCAATAGAACAACGCGGGCGTGTTATTT 300
            |||| ||||| ||| |||||||| |||| ||||||||||||||| |||  ||| ||||||| |
Db      320 GAATACTGTGATGGAGGGGATCTCATGCAAAAGGATCCAGAGCGAGCAGGGAGTGATGTTC 379
Qy      301 AGTGAAGATCAGATCCTCGGTTGTTGGTTGGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360
            ||||||||||||||||| |||||| |||| |||||||  ||||||||||||||  |||||||||||
Db      380 AGCGAAGACCAGATCCTGTGTTGGTTGTACAGATTTCTCTAGGACTGAAGCATATTCAT 439
Qy      361 GACAGGAAGATATATACACAGGGACATAAAGCTCAGACATTTTCTCAGCAAGAACCGA 420
            |||||||| || |||||| ||||||||||| |||||| |||||||| |||||||  ||
Db      440 GACAGGAAGATTTTACACAGGGACATAAAATCCAGAATATTTTCTCAGCAAGAATGA 499
Qy      421 ATGGTGGCAAAGTTGGGGACTTTGGTATAGACGAGTCCTGAATAATTCCATGGAACTT 480
            |||||||| |||||||||||| ||||| |||| |||| ||||| ||| |||| |||||
Db      500 ATGGTTGCCAAGCTCGGGGACTTTGGACAGCAAGAACACTGAATGACTCCATGGAACTT 559
Qy      481 GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCC 540
            |||| |||| | ||||||||||||| |||||| |||||||||||||||||||| |||||
Db      560 GCTCAAACATGTGCTGGCAACCCTTACTACCTGTCCCCAGAGATCTGTCAGAACAGGCCA 619
Qy      541 TACAACAATAAAACGGATATTTGTCTCTTGGGTGTCTTATAGAGTCTGCACACTT 600
            |||||||||||||||| | || |||| ||||| |||||||| ||||||||||||
Db      620 TACAACAATAAAACGGACATCTGGTCCTGGTGTCTTATAGAGTCTGCACACTC 679
Qy      601 AAACATCCTTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACAT 660
            ||||||| ||||||||| |||||| |||||||||| |||| |||||||||||| |||||
Db      680 AAGCATCCTTTTGAGGACAACAACAGTCCACCATCTGGTTCTGAAGATTTGTCAAGGAGT 739
Qy      661 TTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCCTCAGCTCTTT 720
            ||||||| ||| ||||| || || |||| |||||| ||| || ||  |||| |||||||
Db      740 GTTGCTCCCATACACCCCACTTCTCCGTGACCTACAGTCTTCAGTACCCTCAGCTCTTC 799
Qy      721 CAAGTATCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCCTTTTTAGAG 780
            |||||| |||||||||| ||| ||||| ||  |||| |||| |||||||| ||||| ||
Db      800 AGAGTGTCCTCCTCCAGGACCGCATCCGTTACGTGTCCCCTTTGAAAAGACCCTTTTTAGAA 859
Qy      781 AATCTTATTCCCAAATATTGACTCCTGAGGTC-ATTCAGGAAGAATTCAGTCACATGCT 839
            |||| |||| || |||| | ||||| |||||| ||||| ||||| || |||| |||| |
Db      860 ACTTCCATTGCCCGATCCTTGTATCCTGAGGTCTGTTCAGAAGAATCCAGTCCACGCT 919
Qy      840 TATATGCAGGAGCAGGAGCGGCCAGCTTCTCGGACACTGCTGGGAAGGTGGTCCA 890
            ||| ||||||| |||| || ||||  || | ||||| |||| ||||||||||||
Db      920 CACATGGAGGAACATGGCCATTGGCCCCCACCAGCTTGTTGTGGAGAGTTAGTCCA 970
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RESULT 14
AAS11558
ID   AAS11558 standard; cDNA; 3645 BP.
XX
AC   AAS11558;
XX
DT   24-OCT-2001 (first entry)
XX
DE   Human cDNA encoding novel human protein, NHP #2.
XX
KW   Human; novel human protein; NHP; ss; breast cancer; prostate cancer;
KW   immunogen; antibody; gene therapy; antisense.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   CDS              1..3645
FT                    /*tag= a
FT                    /product= "NHP #2"
XX
PN   WO200161016-A2.
```

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XX
PD   23-AUG-2001.
XX
PF   15-FEB-2001; 2001WO-US005356.
XX
PR   18-FEB-2000; 2000US-0183582P.
PR   22-FEB-2000; 2000US-0184014P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Walke DW, Hu Y, Nepomnichy B, Turner CA, Zambrowicz B;
XX
DR   WPI; 2001-502793/55.
DR   P-PSDB; AAU07102.
XX
PT   Isolated nucleic acids encoding novel human proteins useful for the
PT   treatment of disease and as probes for testing and detection.
XX
PS   Disclosure; Page 35-37; 69pp; English.
XX
CC   The invention relates to novel human proteins (NHP) and the nucleic acids
CC   encoding them. The nucleic acids encode mammalian transporter proteins
CC   and are useful for the treatment. (e.g. by gene therapy or antisense
CC   technology) of any of a wide variety of symptoms associated with
CC   biological disorders (e.g. breast and prostate cancer) or imbalances and
CC   as probes for the identification, selection and validation of novel
CC   molecular targets for drug discovery. The proteins may be used to raise
CC   anti-NHP antibodies. The present sequence encodes an NHP of the invention
XX
SQ   Sequence 3645 BP; 1327 A; 594 C; 822 G; 902 T; 0 U; 0 Other;

Query Match   17.9%;   Score 368;   DB 5;   Length 3645;
Best Local Similarity  66.0%;   Pred. No. 1.2e-89;
Matches  549;  Conservative  0;  Mismatches 280;  Indels 3;  Gaps  1;

Qy        1 ATGGATAAGTAGCAGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTA 60
            | |||| ||  ||| ||  ||||||  ||||| || |||||||  |  || ||||  |||||
Db        1 ATGGAGAAGTATGTTAGACTACAGAAGATTGGAGAAGGTTCATTTGGAAAAGCCATTCTT 60

Qy       61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAGAGATCAATTTTGAAAAGATG 120
            ||  ||  || || |||| | ||| |  || | ||  || ||| |||  ||| |||| ||
Db       61 GTTAAATCTACAGAAGATGGCAGCAGTGTATGTTATCAAGGAATTAACATCTCAAGAATG 120

Qy      121 CCCATACAAGAAAAAGAAGCTTCAAAGAAAGAAGTGATTCTCTGAAAAGATGAAACAT 180
            |  |||  ||||||| ||||| |||||  || ||||| | ||||| ||| ||| |||||
Db      121 TCCAGTAAAGAAAGAAAGAGAGAATCAAGGAGGAGAGTTGCAGTATTGGCAAACATGAGCAT 180

Qy      181 CCCAACATTGTAGCCTTCTCTTCAATTCATTCAAGAGAATGGCAGGCGTCTTTATTGTAATG 240
            ||  |||||| |||||||| | | |||||||  |||| || |||   ||||| |||| ||
Db      181 CCAAATATTGTCCAGTATAGAGAATCATTCATTGAAGAAAAATGGCTCTCCTACATAGTAATG 240

Qy      241 GAATATTGTGATGGAGGGGGGGATCCTCGGTTGATGAGGGGATGGGTGTGTTATTT 300
            |||||  ||| ||||| || ||| | |  ||| ||||| |||| ||| |||| ||
Db      241 GATTACTGTGAGGGAGGGGGGGATCGTGTTTAAGCGAATTGTACAGGTTTTTGTTT 300

Qy      301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTCCTCTAGGAGACTAAAACATATTCAT 360
            | || ||| || |||  ||| ||||| ||||| |||   | || || ||| |||| ||||
Db      301 CAAGAGGATCAGCATTTTGGACTGGTTTGTACAGATGTGTTGTACAGACATGTACAT 360

Qy      361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTAGCAAGAACGGA 420
            ||  || || ||  || | ||| |||  |  |  ||| ||| || ||||| ||| ||
Db      361 GATAGAAAAATTCTTCATCGAGACATTAAATCTCGAGACATATTTTAACTAAGATGGA 420

Qy      421 ATGGTGCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
            |||  ||   |||  ||||  || ||||  | | ||  |||  |||  |||| |||
Db      421 ACAGT--ACAACTTGGAGATTTTGGAATTGCTAGAGTTCTTAATAGTACTGTAGAGCTG 477

Qy      481 GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAAGATCTTGTCAGAATAAACCC 540
            ||||| |||| |  ||||| || |||| ||| ||  || |  || |||| ||||| ||| |
Db      478 GCTCGAACTTGCATAGGGACCCCATACTACTTGTCACCTGAAAATCTGAAAACAAACAACCT 537

Qy      541 TACAACAATAAAACGGATATTTCGTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT 600
            ||||  ||||  || |||  || |  || || |||   || || |  | | ||||||
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```
Db      538 TACAATAATAAAAGTGACATTTGGCTCTCGGGTGTGTCCTTTATGAGCTGTGTACACTT 597

Qy      601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGGTTCTCGAAGATTTGTCAAGCACAT 660
            ||||||  | ||||| || |  ||||||||||||||||  ||||||| | |||||| ||||
Db      598 AAACATGCTTTGAGCTGCAGTATGAAAAAACCGGTACTGAAGATAATATCTGGATCT 657

Qy      661 TTTGCCCAATATCTCCGGGGGTTTCTGTGAGCCCATTCCTTGATATCTCAGCTCTTT 720
            ||| |||| ||||| ||||| ||||||| ||||||| ||||||| ||| |||||||||
Db      658 TTTCACCTGTGTCTTTGCATTATTCCATGATCTCCGCAGTTGGTGTCTCAGTTATTT 717

Qy      721 CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTAGAG 780
            ||  |   ||   |||  || ||||  |||  ||| |||  |||   ||  |||| ||
Db      718 AAAAGAAATCCTAGGGATAGACCATCAACTCAGTCCATATTGGAGAAAGGTTTTATAGCC 777

Qy      781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTC 832
            ||| || ||  ||| ||| | ||| || |||||| | ||||||| | |||
Db      778 AAACGCATTGAAAAGTTTCTCTCTCCTCAGCTTATTGCAGAAGAATTTTGTC 829
```

```
RESULT 15
AAL51590
ID   AAL51590 standard; DNA; 3729 BP.
XX
AC   AAL51590;
XX
DT   10-APR-2003  (first entry)
XX
DE   Human serine/threonine protein kinase NEK1 coding sequence #1.
XX
KW   Human; gene; ds; gene therapy; serine/threonine protein kinase; NEK1;
KW   cancer; colon cancer; cardiovascular disorder; congestive heart failure;
KW   central nervous system disorder; chronic obstructive pulmonary disease;
KW   CNS disorder; diabetes; myocardial infarction; ischaemic heart disease;
KW   arrhythmia; hypertensive; Alzheimer's disease; Parkinson's disease;
KW   peripheral pain; chronic pain.
XX
OS   Homo sapiens.
XX
FH            Key          Location/Qualifiers
FT   CDS          1..3729
FT                /tag= a
FT                /product= "Human serine/threonine protein kinase NEK1"
XX
PN   WO2003000873-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-EP006879.
XX
PR   25-JUN-2001; 2001US-0300071P.
PR   16-NOV-2001; 2001US-0331447P.
PR   07-DEC-2001; 2001US-0336693P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; 2003-201424/19.
DR   P-PSDB; AAO16440.
XX
PT   New serine/threonine protein kinase NEK1 gene and protein, useful for
PT   identifying modulators of serine/threonine protein kinase NEK1 activity,
PT   and in gene therapy for treating cancer, diabetes, heart failure or
PT   Alzheimer's disease.
XX
PS   Claim 1; Fig 1; 156pp; English.
XX
CC   The invention comprises the amino acid and coding sequence of the human
CC   serine/threonine protein kinase NEK1. The DNA and protein sequences of
CC   the invention are useful for modulating the activity of serine/threonine
CC   kinase NEK1 in a disease, such as: cancer (particularly colon cancer);
CC   cardiovascular disorders; central nervous system (CNS) disorders;
CC   diabetes; and chronic obstructive pulmonary disease. In particular the
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CC   DNA and protein sequences of the invention are useful for treating:
CC   congestive heart failure; myocardial infarction; ischaemic heart disease;
CC   arrhythmia; hypertensive; Alzheimer's disease; Parkinson's disease; and
CC   peripheral or chronic pain. The present DNA sequence encodes the human
CC   serine/threonine protein kinase NEK1 of the invention
XX
SQ   Sequence 3729 BP; 1358 A; 611 C; 849 G; 911 T; 0 U; 0 Other;

Query Match              17.9%;  Score 368;  DB 8;  Length 3729;
Best Local Similarity    66.0%;  Pred. No. 1.2e-89;
Matches   549;  Conservative   0;  Mismatches  280;  Indels   3;  Gaps   1;

Qy     1 ATGGATAAGTACGATGGATGTGATTAAGGCCATCGGGCAAGGTGCCTCCGGGAAAGCATACTTA 60
         ||||| ||||| |  ||  | |||  | | | || |||||  ||||   |   ||| ||| | |
Db     1 ATGGAGAAGTATGTTAGACTACAGAAGATTGGAGAAGGTTCATTTGGAAAAGCCATTCTT 60

Qy    61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG 120
         | |||   | ||| || |  ||  | |||  |  ||||| |||| ||| | |||||| |||
Db    61 GTTAAATCTACAGAAGATGGCAGCAGTAGTATGTTATCAAGGAAATTAACATCTCAAGAAATG 120

Qy   121 CCCATACAACAGAAAAAGAAGTTCAAAGAAGAAGTGATTCTTCTGGAAAAGATGAAACAT 180
          |   |  | || |||||| | |   |||||||| ||   |  ||  ||| ||||| |||
Db   121 TCCAGTAAAGAAAGAAGAGAATCAAGGAGAGAAGTTGCAGTATTGGCAAACATGAAGCAT 180

Qy   181 CCCAACATTGTAGCCTTCTCAATTCATTCAAGAGAATGGCAGGCTGTTATTGTAATG 240
          | ||| ||||  | || || |||||||  ||||| ||| |  | |||| |  |||
Db   181 CCAAATATTGTCCAGTATAGAATCATTTGAAGAAAATCATTGGCTCTCTCTACATAGTAATG 240

Qy   241 GAATATTGTGATGGAGGGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATTT 300
         ||| | ||| | ||||||||||||| | | ||| | | | ||| |||  |  | ||||||||
Db   241 GATTACTGTGAGGGAGGGGGATCTCGTTGTGTTAAGCGAATAAAATGCTCAGAAAGGCGTTTTGTTT 300

Qy   301 AGTGAAGATCAGATCCTCGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360
           |||| |||||||  |  | |||| |||||||| |   | | ||  | || ||||| ||
Db   301 CAAGAGGATCAGATTTTGGACGTGGTTTGTACAGACATTGTTGGCCCTGAAACATGTACAT 360

Qy   361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTTCTTAGCAAGAACGGA 420
         || |  ||  |||  ||| | ||||| ||| ||||||||| ||  | ||   |||| ||
Db   361 GATGAAAAAATTCCTTCATCGAGACATTAAAATCTCAGAACACATATTTTTAACTAAAGATGGA 420

Qy   421 ATGGTGGGCAAAGCTTGGGAGCTTTGGTATAGCAAGAGTCCGAATAATTCCATGGAACTT 480
         | ||  ||| ||||| |||| ||||||| | ||||||||| ||||||| | || ||| ||
Db   421 ACAGT---ACAACTTGGAGATTTTGGAATTGCTAGAGTTCTTAATAGTACTGTGAGAGCTG 477

Qy   481 GCTCGAACTTGTATTGGAACACACTTCCCCAGAGATCTGTCAGAATAAACCC 540
         |||||||||||  | ||| |||| | |  ||||| ||| ||| || ||| ||
Db   478 GCTCGAACTTGCATAGGGACCCCATACTACTTGTCAAATCTGAAAATCAAACCT 537

Qy   541 TACAACAATAAAACCGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT 600
         |||||  ||||||   ||||||||| |||| || |||||| | |||||||| ||  | ||
Db   538 TACAATAATAAAAGTGACATTTGGCCTCTGGGGTGTGTCCTTTATGAGCTGTGTACACTT 597

Qy   601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTCGAAGATTTGTCAAGCACAT 660
         |||||| ||||| | | | || | || | ||  || ||  |||||||| | |||| |||
Db   598 AAACATGCTTTGAAGCTGGAAGCTGGCTACTGAAGATAATATCTGGATCT 657

Qy   661 TTTGCCCCAATATCTCCGGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720
         ||| | ||  | |||| ||  | | ||  | | | |||| |  ||  |||||||| | |||
Db   658 TTTCCACCTGTGTCTTTGCATTATTCCTATGATCTCCGCAGTTTGGTGTCTCAGTTATTT 717

Qy   721 CAAGTATCCCTCGAGACCGACCATCCATAAAATTCCATTTTGAAAAGGCCCCTTTTTAGAG 780
         ||| || |||  ||| | || ||||  ||||  || ||  | |||||| ||| |||| ||
Db   718 AAAAGAAATCCTAGGGATAGACCATCAGCTCAACTCCCATATTGGAGAAGGTTTTATAGCC 777

Qy   781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGGAAGAATTCAGTC 832
         ||| | |||  | |||   |  || | ||| | ||| | || |||||||| | |||
Db   778 AAACGCCATTGAAAAGTTTCTCTCCTCAGCTTATTGCAGAAGAATTTTGTC 829
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                 Copyright    GenCore version 5.1.6
                 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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        14:  /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	Length	ID	Description
1	2052	100.0	2052	9	2052	US-09-940-921B-1	Sequence 1, Appli
2	2052	100.0	2240	9	2240	US-09-940-921B-5	Sequence 5, Appli
3	1868	91.0	1965	9	1965	US-09-940-921B-3	Sequence 3, Appli
4	1654	80.6	2370	14	2370	US-10-243-735-1	Sequence 1, Appli
5	1654	80.6	2370	14	2370	US-10-730-010-1	Sequence 1, Appli
6	1190.2	58.0	1587	16	1587	US-10-114-270-187	Sequence 187, App
7	1178.4	57.4	1453	16	1453	US-10-114-270-185	Sequence 185, App
8	368	17.9	3645	9	3645	US-09-783-320-3	Sequence 3, Appli
9	368	17.9	5426	9	5426	US-09-783-320-50	Sequence 50, Appl
10	368	17.9	5448	15	5448	US-10-037-270-246	Sequence 246, App
11	368	17.9	5448	15	5448	US-10-117-722-246	Sequence 246, App
12	368	17.9	5532	15	5532	US-10-037-270-245	Sequence 245, App
13	368	17.9	5532	15	5532	US-10-117-722-245	Sequence 245, App
14	260.8	12.7	1588	16		US-10-114-270-181	Sequence 183, App
15	259.2	12.6	1781	16		US-10-114-270-181	Sequence 181, App
16	259.2	12.6	2257	16		US-10-114-270-179	Sequence 179, App
17	252.8	12.3	2110	16		US-10-415-011-29	Sequence 29, Appl
18	238.4	11.6	1846	9		US-09-870-962-15	Sequence 15, Appl
19	205.2	10.0	63588	14		US-10-243-735-3	Sequence 3, Appli
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23	170.2	8.3	1528	15		US-10-288-798-47	Sequence 47, Appl
24	170.2	8.3	1528	16		US-10-362-892-47	Sequence 47, Appl
25	170.2	8.3	2079	9		US-09-992-48-1	Sequence 1, Appli
26	170.2	8.3	2079	15		US-10-434-034-1	Sequence 1, Appli
27	170.2	8.3	2142	14		US-10-162-706-1	Sequence 1, Appli
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33	168.4	8.2	2940	9		US-09-884-001-3	Sequence 3, Appli
34	167.4	8.1	3696	17		US-10-620-052A-31	Sequence 31, Appl
35	166.8	8.1	2940	15		US-10-372-736-1	Sequence 1, Appli
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37	165.8	8.1	3544	16		US-10-425-114-26260	Sequence 26260, A
38	165.8	8.1	3544	16		US-10-425-114-26275	Sequence 26275, A
39	165.8	8.1	3698	15		US-10-172-118-880	Sequence 880, App
40	165.8	8.1	3698	16		US-10-342-887-880	Sequence 880, App
41	159.4	7.8	1219	9		US-09-822-849A-371	Sequence 371, App
42	150.4	7.3	1680	15		US-10-288-798-46	Sequence 46, Appl
43	150.4	7.3	1680	16		US-10-362-892-46	Sequence 46, Appl
44	136.4	6.6	993	10		US-09-898-837A-8	Sequence 8, Appli
45	136	6.6	357	16		US-10-242-535A-8834	Sequence 8834, Ap

ALIGNMENTS

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RESULT 1
US-09-940-921B-1
;  Sequence 1, Application US/09940921B
;  Patent No. US2002014732A1
;  GENERAL INFORMATION:
;  APPLICANT: Friddle, Carl Johan
;  APPLICANT: Hilbun, Erin
;  APPLICANT: Nepomnichy, Boris
;  APPLICANT: Hu, Yi
;  TITLE OF INVENTION: No. US20020147320A1el Human Kinase Proteins and Polynucleotides 1
;  FILE REFERENCE: LEX-0227-USA
;  CURRENT APPLICATION NUMBER: US/09/940,921B
;  CURRENT FILING DATE: 2002-05-21
;  PRIOR APPLICATION NUMBER: US 60/229,280
;  PRIOR FILING DATE: 2000-08-31
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 1
;  LENGTH: 2052
;  TYPE: DNA
;  ORGANISM: homo sapiens
US-09-940-921B-1

Query Match             100.0%;  Score 2052;  DB 9;  Length 2052;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 2052;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy 1261 GTGGAGAAGCAATTGGGTCTTCGTCGTCTCTGCCGAGCCAAATTACAACCAGAGACAA   1320
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Db 1861 CAGACTGTAGTGCTGTGGGAAACAGGAGGCAGTGGGATGGAGGAGGCGCCTCAGACTCTG 1920

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Qy 2041 ATCCTGATGTGA 2052
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RESULT 2
US-09-940-921B-5
; Sequence 5, Application US/099940921B
; Patent No. US2002147320A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: No. US2002147320A1e1 Human Kinase Proteins and Polynucleotides E...
; FILE REFERENCE: LEX-0227-USA
; CURRENT APPLICATION NUMBER: US/09/940,921B
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/229,280

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Db 181   CCCAACATTGTAGCCTTCTTCAATTCATTTCAATTCAAGAGAGAATGGCAGGCTGTTTATTGTAATG 240

Qy 241   GAATATTGTGATGGAGGGGATCCATGAAAAAGGATCAATAGACAACGGGGTGTGTTATTT 300
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Qy 301   AGTGAAGATCAGATCCTCCGGTTGGTTTGTACAGATTCTCTAGGACTAAAAACATATTCAT 360
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Qy 361   GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAGACATTTTTCTTAGCAAGAACGGA 420
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Db 421   ATGGTGGCAAAGCTTGGGACTTTGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT   480

Qy 481   GCTCGAACTTGTATTGGAACACTTACTACCTGTCCCCAGAGATCTGTCGCAGAATAAACCC 540
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Db 541   TACAACAATAAAACGGATATTTGGTCCTTGGCTCTTGTATATGGCTCCTGCCACACTT   600

Qy 601   AAACATCCTTTGAGGGTAACAACTTACAGCAGCAGCTGGTTCTGAAGATTGTTCAAGCACAT 660
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Db 601   AAACATCCTTTGAGGGTAACAACTTACAGCAGCAGCTGGTTCTGAAGATTGTTCAAGCACAT 660

Qy 661   TTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGTCTCTT   720
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Db 661   TTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGTCTCTT   720

Qy 721   CAAGTATCTCCTCGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTGAGAG 780
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Qy 781   AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT 840
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Qy 841   ATATGCAGCAGCAGGAGCCGCCAGCTTCTCGGGAAGTGGTCCAGGAAGTGTAAA   900
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Qy 1141 CCTTCAAGAGAAAATACTGGAGTTGAGGATTGAGGAGGCATGGTCCATCCCCA   1200
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; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2240
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-940-921B-5

Query Match      100.0%;   Score 2052;   DB 9;   Length 2240;
Best_Local Similarity   100.0%;   Pred. No. 0;
Matches 2052;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy  241 GAATATTGTGATGAGGAGATCCATGAAAAGAATCAATAGACAACGGGTGTGTTATTT       300
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Db  345 GAATATTGTGATGAGGAGATCCATGAAAAGAATCAATAGACAACGGGTGTGTTATTT       404

Qy  301 AGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTTCTACAGACTAAAACATATTCAT      360
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Db  405 AGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTTCTACAGACTAAAACATATTCAT      464

Qy  361 GACAGGAAGATATTACACAGGGACATGGACACATAAAGCTCAGAACATTTTCTTAGCAAGAACCGA   420
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Db  465 GACAGGAAGATATTACACAGGGACATGGACACATAAAGCTCAGAACATTTTCTTAGCAAGAACCGA   524

Qy  421 ATGGTGGCAAAGCTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT    480
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Db  525 ATGGTGGCAAAGCTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT    584

Qy  481 GCTCGAACTTGTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCGTGAATAAACCC  540
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Db  585 GCTCGAACTTGTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCGTCAGAATAAACCC  644

Qy  541 TACAACAATAAAACGATATTTGGTCTCTTGGCTGTCTTATATGAGCTCTGCACACTT      600
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Db  645 TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTCTTATATGAGCTCTGCACACTT      704

Qy  601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAAGCACAT     660
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Db  705 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAAGCACAT     764

Qy  661 TTTGCCCAATATCTCCGGGGGTTTCTCGTGAGCTCCATTCCATTTGAAAAGGCCCTTTT     720
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Db  765 TTTGCCCAATATCTCCGGGGGTTTCTCGTGAGCTCCATTCCATTTGAAAAGGCCCTTTT     824

Qy  721 CAAGTATCCTCGAGACCGACCATCCATAAATTTCAATTTGAAAAGGCCCTTTTTAGAG     780
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Db  825 CAAGTATCCTCGAGACCGACCATCCATAAATTTCAATTTGAAAAGGCCCTTTTTAGAG     884

Qy  781 AATCTTATTCCCAAATATATTTGACTTCCTGAGGTCATTCAGGAAGAAGAATTCAGTCACATGCTT    840
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Qy  841 ATATTGCAGAGCAGGAGCGCGCCAGCTTCTCCGACATGCTCGGGAAGGTGGTCCAGAAGTGTAAA   900
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Qy  901 ATACAAAAAGTGAGATTCCAGGGAAAGTGCCCACCAGGAAGTCAAGGAAGATCTTATGATTAT   960
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Db 1005 ATACAAAAAGTGAGATTCCAGGGAAAGTGCCCACCAGGAAGTCAAGGAAGATCTGTGTGCCAATT  1064

Qy  961 AAAGGAATGCTATATTGCATAGAAATGAATGAGAAATGAATGAGACCACCACGTCCTCGTGTGACC  1020
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Db 1245 CCTCAAGAAAATACTGGAGTTGAGGTTGAGGATTACGGTCAGGACGATGGTCATCCCCCA  1304

Qy 1201 AGTCAATGGCCTGCTGAGTACCTTCAGAGAAAATTTGAAGCTCAACAATATAAGTTGAAA  1260
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Db 1305 AGTCAATGGCCTGCTGAGTACCTTCAGAGAAAATTTGAAGCTCAACAATATAAGTTGAAA  1364

Qy 1261 GTTGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1365 GTTGGAGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA  1424

Qy 1321 GAGCTAAGAAGTAATGAGAAGAGCCTAGATTCCAGGAGAGAGAATCCAGGAGAAAAACGAA  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1425 GAGCTAAGAAGTAATGAGAAGAGCCTAGATTCCAGGAGAGAGAATCCAGGAGAAAAACGAA  1484

Qy 1381 ATGAAGAACACAGAATATTGGAAGCAGCAGTTAGAAGCAGTACGCACCACCAATGAC  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1485 ATGAAGAACACAGAATATTGGAAGCAGCAGTTAGAAGCAGTACGCACCACCAATGAC  1544

Qy 1441 ATGAAAGAAATTAGAAAGAAGAATTAGAAGCAACCAGAGAGAACTCAAAAATAAGTCAT  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1545 ATGAAAGAAATTAGAAAGAAGAATTAGAAGCAACCAGAGAGAACTCAAAAATAAGTCAT  1604

Qy 1501 AAACCTATTTGTGAAGAAGTAACCTGCCTGTCATCAAGATGCATCTGAGGGGAGAA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1605 AAACCTATTTGTGAAGAAGTAACCTGCCTGTCATCAAGATGCATCTGAGGGGAGAA  1664

Qy 1561 GCACCTGTGCAGACAACTTGAAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGAA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1665 GCACCTGTGCAGACAACTTGAAAAAGACTTGAAACAAATGAGGCTTCAGAACAACAAAGAA  1724

Qy 1621 AGTAAAAATCCAGAACAGAAAAATAAAGCTAAGAAGGGGGTAAAATTGAAATTAATTTA  1680
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Db 1725 AGTAAAAATCCAGAACAGAAAAATAAAGCTAAGAAGGGGGTAAAATTGAAATTAATTTA  1784

Qy 1681 GACAAATGTATTTCTGATGAAACATCCTCAAGAGAGAAGAGGCAATGGATATATACCAAAT  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1785 GACAAATGTATTTCTGATGAAACATCCTCAAGAGAGAAGAGGCAATGGATATATACCAAAT  1844

Qy 1741 GAAACTTTGACCTTGAGGATGCATGAAGTTTAAGGAATGTGTAAAGGAGCAT  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1845 GAAACTTTGACCTTGAGGATGCATGAAGTTTAAGGAATGTGTAAAGGAGCAT  1904

Qy 1801 GGAGATTATACAGACAAAGCATTTGAAAAACTTCACTGCCCAGAAGCAGGGTTTTCCACG  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1905 GGAGATTATACAGACAAAGCATTTGAAAAAACTTCACTGCCCAGAAGCAGGGTTTTCCACG  1964

Qy 1861 CAGACTGTAGCTGCTGTGTGTGAAACAGGAGGCAGTGGATGGAGGAGGCGCCTCAGACTCTG  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1965 CAGACTGTAGCTGCTGTGTGTGAAACAGGAGGCAGTGGATGGAGGAGGCGCCTCAGACTGTG  2024

Qy 1921 CTGCAGATGATGGCAGTGGCCGACATCGCCGACATCACCTGCCCCACGGGCCTGACAGTGAG  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2025 CTGCAGATGATGGCAGTGGCCGACATCGCCGACATCACCTGCCCCACGGGCCTGACAGTGAG  2084

Qy 1981 TCTGTGCTTAGCGTCAGTCGTCAGGAAGAGTCTGGAAGTGTAAA  2040
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Db 2085 TCTGTGCTTAGCGTCAGTCGTCAGGAAGGGAGGGAAGAGACCAAGGACCCGTACAGCCCAGTGCTC 2144
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 2041 ATCCTGATGTGA 2052
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Db 2145 ATCCTGATGTGA 2156

RESULT 3
US-09-940-921B-3
; Sequence 3, Application US/09940921B
; Patent No. US20020147320A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: No. US20020147320A1e1 Human Kinase Proteins and Polynucleotides E
; FILE REFERENCE: LEX-0227-USA
; CURRENT APPLICATION NUMBER: US/09/940,921B
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/229,280
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
US-09-940-921B-3
; SEQ ID NO 3
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: homo sapiens

Query Match   91.0%; Score 1868; DB 9; Length 1965;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 1965; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

Qy   1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCAAGTGCCTTCGGGAAAGCATACTTA 60
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Db   1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCAAGTGCCTTCGGGAAAGCATACTTA 60

Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG 120

Qy 121 CCCATACAAGAAAAAGAAGAGCTTCAAAGAAGAAGTGATTCTTCTGAAAGATGAAACAT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CCCATACAAGAAAAAGAAGAGCTTCAAAGAAGAAGTGATTCTTCTGAAAGATGAAACAT 180

Qy 181 CCCAACATTGTAGCCTTCTTCAATTCATTGCAGGAGAAGGTGTTTATTGTTAATG 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 CCCAACATTGTAGCCTTCTTCAATTCATTGCAGGAGAAGGTGTTTATTGTTAATG 240

Qy 241 GAATATTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACAACGGGGTGTTATTT 300
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Db 241 GAATATTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACAACGGGGTGTTATTT 300

Qy 301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTTCTCTAGGAGACTAAAACATATTCAT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTTCTCTAGGAGACTAAAACATATTCAT 360

Qy 361 GACAGGAAGATATTACACAGGGACATAAAAGTCAGAACATTTTCTTCAGCAAGAACGGA 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GACAGGAAGATATTACACAGGGACATAAAAGTCAGAACATTTTCTTCAGCAAGAACGGA 420

Qy 421 ATGGTGGCAAAGTTGGGGACTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
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Db 421 ATGGTGGCAAAGTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480

Qy 481 GCTCGAACTTGTATTGGAACACCTTACCTGTCCCCGAGATCTGTCAGAATAAACCC 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 GCTCGAACTTGTATTGGAACACCTTACCTGTCCCCGAGATCTGTCAGAATAAACCC 540

Qy 541 TACAACAATAAAACGGATATTTGGTCTTCTTGGCTGTGTCTTATGAGCTCTGCACACTT 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 TACAACAATAAAACGATATTTGGTCTTCTTGGCTGTGTCTTATGAGCTCTGCACACTT 600

Qy 601 AAACATCCTTTGAGGGTAACAACTTACACGCAGCAGTGGTTCTGAAGATTTGTCAAGCACAT 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 AAACATCCTTTGAGGGTAACAACTTACACGCAGCAGTGGTTCTGAAGATTTGTCAAGCACAT 660

Qy 661 TTTGCCCCAATATCTCCGGGGTTTTCGTGAGCTCCATTCCTGAGTATCTCAGCTCTT 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 TTTGCCCCAATATCTCCGGGGTTTTCGTGAGCTCCATTCCTGAGTATCTCAGCTCTT 720

Qy 721 CAAGTATCTCCGAGACCGACCATCCATAAATTCCATTTTGAAAAGGCCCTTTTTAGAG 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 CAAGTATCTCCGAGACCGACCATCCATAAATTCCATTTTGAAAAGGCCCTTTTTAGAG 780

Qy 781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT 840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTCACATGCTT 840

Qy 841 ATATGCAGAGCAGGAGCGCCAGCTTCTCCGACATGCTGGGAAGGTGGTCCAGAAGTGTAAA 900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 ATATGCAGAGCAGGAGCGCCAGCTTCTCCGACATGCTGGGAAGGTGGTCCAGAAGTGTAAA 900

Qy 901 ATACAAAAGTGAGATTCCAGGGAAAGTGCCCACCCAAGATCAAGAGATCTGTGCCAATT 960
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Db 901 ATACAAAAGTGAGATTCCAGGGAAAGTGCCCACCCAAGATCAAGAGATCTGTGCCAATT 960

Qy 961 AAAAGGAATGTATATTGCATAGAAATGAATGAGACACCAGCTGGAGCCAGAAGGCC 1020
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 AAAAGGAATGTATATTGCATAGAAATGAATGAGACACCAGCTGGAGCCCAGAAGGCC 1020

Qy 1021 AGATCTATAAAAATGATAGAAAAGACCCAAAATTGCTGCTGTCTGTGGACATTATGATTAT 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 AGATCTATAAAAATGATAGAAAAGACCCAAAATTGCTGCTGTCTGTGGACATTATGATTAT 1080

Qy 1081 TATTATGCTCAACTTGATATGCTGAGGAGTTGAGGATTACGGTCAAGGCATGGTCATCCCCA 1140
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Db 1081 TATTATGCTCAACTTGATATGCTGAGGAGTTGAGGATTACGGTCAAGGCATGGTCATCCCCA 1140

Qy 1141 CCTCAAGAAAATACTGGAGTTGAGGTTACGGTCAGGAGAAACGAGGCATGGTCCATCCCCA 1200
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 CCTCAAGAAAATACTGGAGTTGAGGTTACGGTCAGGAGAAACGAGGCATGGTCCATCCCCA 1200

Qy 1201 AGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAAA 1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 AGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAAA 1260

Qy 1261 GTGGGAAGCAATGGGTCTTCGTCGTCAGACATTTCTGCGGCCAAATTACAACCAGAGACA 1320
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 GTGGGAAGCAATGGGTCTTCGTCGTCCATCTTCTGCGGCCAAATTACAACCAGAGACA 1320

Qy 1321 GAGCTAAGAGTAATGGAGAAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAGAAAACGAA 1380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 GAGCTAAGAGTAATGGAGAAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAGAAAACGAA 1380

Qy 1381 ATGAGGAACAGGAATATTGGAAGCAGTCAGTGAGAAATACGCCAACAGTACCACAATGAC 1440
        ||||||||||||
Db 1381 ATGAGGAAC-- 1390

Qy 1441 ATGAAAGAAATTAGAAGAAGATGGGAGAGAACCAGAGGAACTCAAAAATAAGTCAT 1500
                                              ||||||||||||||||||||
Db 1391 ------------------------------AGGAGAACTCAAAAATAAGTCAT 1413

Qy 1501 AAAACCTATTTGGTGAAGAAGAGTAACCTTGCCTGTCCATCAAGATGCATCTGAGGGAGAA 1560
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1414 AAAACCTATTTGGTGAAGAAGAGTAACCTTGCCTGTCCATCAAGATGCATCTGAGGGAGAA 1473

Qy 1561 GCACCTGTGCAGGACATTGAACAAATGAGACTTGAAACAAATGAGACTTCAGACACAAAGGAA 1620
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1474 GCACCTGTGCAGGACATTGAACAAATGAGACTTGAAACAAATGAGACTTCAGACACAAAGGAA 1533

Qy 1621 AGTAAAAAATCCAGAACAGAAAATATAAAGCTAAAGCTAAGGGGTAAAATTTGAAATTAATTTA 1680
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1534 AGTAAAAAATCCAGAACAGAAAATATAAAGCTAAGGGGTAAAATTTGAAATTAATTTA 1593

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Qy    301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    312 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 371

Qy    361 GACAGGAAGATATTACACAGGGACATAAAGTCAGAACATTTTCTTAGCAAGAACGGA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 GACAGGAAGATATTACACAGGGACATAAAGTCAGAACATTTTCTTAGCAAGAACGGA 431

Qy    421 ATGGTGGCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATATTCCATGGAACTT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    432 ATGGTGGCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATATTCCATGGAACTT 491

Qy    481 GCTCGAACTTGTATTGGAACACCTTACCTTGTCCCCAGAGATCGTCTGCAGAATAAACCC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    492 GCTCGAACTTGTATTGGAACACCTTACCTTGTCCCCAGAGATCGTCTGCAGAATAAACCC 551

Qy    541 TACAACAATAAAACGGTATATTGTCTTCTTGGCTGTCTTATATGAGCTCTGCACACTT 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    552 TACAACAATAAAACGGTATATTGTCTTCTTGGCTGTCTTATATGAGCTCTGCACACTT 611

Qy    601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGAGATTTGTCAGCACAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    612 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGAGATTTGTCAGCACAT 671

Qy    661 TTTGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    672 TTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 731

Qy    721 CAAGTATCTCCTCGAGACCGACCACTCCATCCATAAATTCCATTTGAAAAAGGCCCTTTTTAGAG 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    732 CAAGTATCTCCTCGAGACCGACCACTCCATCCATAAATTCCATTTGAAAAAGGCCCTTTTTAGAG 791

Qy    781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGAATTCAGTCACATGCTT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    792 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGAATTCAGTCACATGCTT 851

Qy    841 ATATGCAGAGCAGGAGGCGCGCCAGCTTCTCGACATGCTGGGAAGTGGTCCAGAAGTGTAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 ATATGCAGAGCAGGAGGCGCGCCAGCTTCTCGACATGCTGGGAAGTGGTCCAGAAGTGTAAA 911

Qy    901 ATACAAAAAGTGAGATTCCAGGGAAAGTGCCACCAAGATCAAGGAGATCTGTGCCAATT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    912 ATACAAAAAGTGAGATTCCGGGGAAAGTGCCACCAAGATCAAGGAGATCTGTGCCAATT 971

Qy    961 AAAAGGAATGCTATATTGCATAGAAATGATAGAAGACCCAAAATTGCTCGTGTCTGTGGGAAGGCC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    972 AAAAGGAATGCTATATTGCATAGAAATGATAGAAGACCCAAAATTGCTCGTGTCTGTGGGAAGGCC 1031

Qy   1021 AGATCTATAAAAATGATAGAAAGACCCAAAATTGCTGCTGTGTGTGGACATTATGATTAT 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 AGATCTATTAAAAATGATAGAAAGACCCAAAATTGCTGTGTCTGTGTGGGACATTATGATTAT 1091

Qy   1081 TATTATGTCTCAACTTGATATGCTGAGGAGGAGCCCACAAACCAAGTTATCACCCTATT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1092 TATTATGTCTCAACTTGATATGCTGAGGAGGAGCCCACAAACCAAGTTATCACCCTATT 1151

Qy   1141 CCTTCAAGAAAAATACTGAGGTTGAGGATTACGGTCAGGAGAAACGAGGCATGGTCCATCCCCA 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1152 CCTTCAAGAAAAATACTGGAGTTGAGGATTACGGTCAGGAGAAACGAGGCATGGTCCATCCCCA 1211

Qy   1201 AGTCAATGGCCTGCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAAA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 AGTCAATGGCCTGCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAAA 1271

Qy   1261 GTGGAGAGCAATTGGGCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 GTGGAGAGCAATTGGGCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACAA 1331

Qy   1321 GAGCTAAGAAGTAATGCAGGATCTCATGAAAAGAGAATCAATAGACAACGGGGTGTGTATTT 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1332 GAGCTAAGAAGTAATGCAGGATCTCATGAAAAGAGGATCAATAGACAACGGGGTGTGTTATTT 1391
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Qy   1681 GACAAATGTATTCTGATGAAACATCCTCCAGAGAGGAAGAGGCAATGATATACCAAAT 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1594 GACAAATGTATTCTGATGAAACATCCTCCAGAGAGGAAGAGGCAATGATATACCAAAT 1653

Qy   1741 GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGAATGTGTAAAGGAGCAT 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1654 GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGAATGTGTAAAGGAGCAT 1713

Qy   1801 GGAGATTATACAGACAACAAAGCATTTGAAAAACTTCACTGCCCAGAAGCAGGGTTTCCACG 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1714 GGAGATTATACAGACAACAAAGCATTTGAAAAACTTCACTGCCCAGAAGCAGGGTTTCCACG 1773

Qy   1861 CAGACTGTAGCTGCTGTGGGAAACAGGAGGCAGTGGGATGGAGGAGCGCCTCAGACTCTG 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1774 CAGACTGTAGCTGCTGTGGGAAACAGGAGGCAGTGGGATGGAGGAGCGCCTCAGACTCTG 1833

Qy   1921 CTGCAGATGATGGCAGTGGCTGCCGACATCACCTCACCTCGGGCCTGACAGTGAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1834 CTGCAGATGATGGCAGTGGCTGCCGACATCACCTCACCTCCACCGGGCCTGACAGTGAG 1893

Qy   1981 TCTGTGCTTAGCGTCAGTCGTCAGGAAGGGAAGACCAAGGACCCGTACAGCCCCAGTGCTC 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1894 TCTGTGCTTAGCGTCAGTCGTCAGGAAGGGAAGACCAAGGACCCGTACAGCCCCAGTGCTC 1953

Qy   2041 ATCCTGATGTGA 2052
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Db   1954 ATCCTGATGTGA 1965
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RESULT 4
US-10-243-735-1

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; Sequence 1, Application US/10243735
; Publication No. US20030022341A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001212DIV
; CURRENT APPLICATION NUMBER: US/10/243,735
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: Human
US-10-243-735-1
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Query Match   80.6%;   Score 1654;   DB 14;   Length 2370;
Best Local Similarity   94.5%;   Pred. No. 0;
Matches 1763;   Conservative   0;   Mismatches   10;   Indels   93;   Gaps   1;

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Qy      1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCCATACTTA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCCATACTTA 71

Qy     61 GCTAAAGGGAAATCAGATAGCAAGCACTGTTGTCATAAAGAGATCAATTTTGAAAAGATG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72 GCTAAAGGGAAATCAGATAGCAAGCACTGTTGTCATAAAGAGATCAATTTTGAAAAGATG 131

Qy    121 CCCATACAAGAAAAGAGCTTCAAAGAAAGAGTGATTCTTCTGGAAAAGTGAAACAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 CCCATACAAGAAAAGAGCTTCAAAGAAAGAGTGATTCTTCTGGAAAAGTGAAACAT 191

Qy    181 CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGAATGGCAGGCTGTTTATTGTAATG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    192 CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGAATGGCAGGCTGTTTATTGTAATG 251

Qy    241 GAATATTGTGATGGAGGGGATCTCATGAAGAAAAGGATCAATAGACAACGGGGTGTGTATTT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 GAATATTGTGATGGAGGGGATCTCATGAAGAAAAGGATCAATAGACAACGGGGTGTGTTATTT 311
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Qy  181  CCCAACATTGTAGCCTTCAATTCATTCAGAGAGATGGCAGGCTGTGTTTATTGTAATG  240
         ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  192  CCCAACATTGTAGCCTTCAATTCATTCAGAGAATGGCAGGCTGTGTTTATTGTAATG   251

Qy  241  GAATATTGTGATGGAGGGGATCTCATGAAAAGGATCAATAGACACGGGGTGTGTTATT   300
         |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252  GAATATTGTGATGGAGGGGATCTCATGAAAAGGATCAATAGACACGGGGTGTGTTATTT  311

Qy  301  AGTGAAGATCAGATCATCCGGTTGGTTGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  312  AGTGAAGATCAGATCATCCGGTTGGTTGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT  371

Qy  361  GACAGGAAGATATTACACAGGACATAAAAGCTTCAGAACAACAAAGGAA  420
         ||||||||        |||||||||||||||||||||||||||||||||
Db  372  GACAGGAAG-------ACAGGACATAAAAGCTTCAGAACAACAAAGGAA   431

Qy  421  ATGGTGCAAAGCTTGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  432  ATGGTGCAAAGCTTGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  491

Qy  481  GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCAGAGATCTGTCAGAATAAACCC  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  492  GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCAGAGATCTGTCAGAATAAACCC  551

Qy  541  TACAACAATAAAACGGATATTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  552  TACAACAATAAAACGGATATTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT  611

Qy  601  AAACATCCTTTGAGGGTAACAACTCACGACCAGCTGGTTCTGAAGATTGTCAAGCACAT  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  612  AAACATCCTTTGAGGGTAACAACTCACGACCAGCTGGTTCTGAAGATTGTCAAGCACAT  671

Qy  661  TTTGCCCCAATATCTCCGAGACCGACCATCCATAAATTCATTTGAAAAGGCCCTTTTTAGAG  720
         ||||||||||||||||||||||||||||||||   |||||||||||||||||||||||||||
Db  672  TTTGCCCCAATATCTCCGAGACCGACCATCCATCAATAAATTCATTTGAAAAGGCCCTTTTTAGAG  731

Qy  721  CAAGTATCTCCTGAGACCGACCACCGACCATCCATAAATTCCATTTGAAGAAGGCCCTTTTTAGAG  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  732  CAAGTATCTCCTGAGACCGACCACCGACCATCCAATAAATTCCATTTGAAGAAGGCCCTTTTTAGAG  791

Qy  781  AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGGTGGTCCAGAGTGTAAA  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  792  AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGGTGGTCCAGAGTGTAAA  851

Qy  841  ATATGCAGAGCAGGAGCGCGCCAGCTTCTCGACATGCGGACATGCTGGGAAGGTGGTCCAGAAGTGTAAA  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  852  ATATGCAGAGCAGGAGCGCGCCAGCTTCTCGACATGCGGACATGCTGGGAAGGTGGTCCAGAAGTGTAA   911

Qy  901  ATACAAAAGTGAGATTCCAGGGAAAGTGCCACCAGTGAGCCAAGATATCTGTGCCAATT  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  912  ATACAAAAGTGAGATTCCAGGGAAAGTGCCACCAGTGAGCCAAGATATCTGTGCCAATT  971

Qy  961  AAAAGGAATGCTATATTGCATAGAAATGAATGAAAGACCCAAAATTGCTGCTGTCTGTGGACCATTATGATTAT  1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  972  AAAAGGAATGCTATATTGCATAGAAATGAATGAAAGACCCAAAATTGCTGCTGTCTGTGGACCATTATGATTAT  1031

Qy  1021 AGATCTATAAAAATGATAGAAAGACCCAAAAATTGCTGCTGTCTCTGGACATTATGATTAT  1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1032 AGATCTATAAAAATGATAGAAAGACCCAAAAATTGCTGCTGTCTCTGGACATTATGATTAT  1091

Qy  1081 TATTATGCTCAACTTGATATGCTGATATGCTGAGCGAGGAGCGAGGAGCATCACCCTATT  1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1092 TATTATGCTCAACTTGATATGCTGATATGCTGAGCGAGGAGCGAGGAGCATCACCCTATT  1151

Qy  1141 CCTCAAGAAAATACTGGAGTTGACGATTACGGTCAGGAAAGCATGTCCATCCCCA  1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1152 CCTCAAGAAAATACTGGAGTTGACGATTACGGTCAGGAAAGCATGTCCATCCCCA  1211

Qy  1201 AGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAAA  1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1212 AGTCAATGGCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAAA  1271

Qy  1261 GTGGAGAAGCAATTGGTCTTCGTCCATCTTCGTCCGAGCCAATTACAACCAGAGACAA  1320
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Qy  1381 ATGAAGGAACAGAGAATATTGGAGCAGCAGTTAGAGGAGGAAATACGCGCCAACAGTACCACAATGAC  1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1392 ATGAAGGAACAGAGAATATTGGAGCAGCAGTTAGAGGAGGAAATACGCGCCAACAGTACCACAATGAC  1451

Qy  1441 ATGAAAGAAATTAGAAGAAGATGGGGAGAGAACCAGGAGAACTCAAAATAAGTCAT  1500
         ||||||||||||||||||||||||||||||||||||||
Db  1452 ATGAAAGAAATTAGAAGAAGATGGGGAGAGAACCAG-------------------  1488

Qy  1501 AAAACCTATTTGTGAAGAAGTAACCTGCCTGTCCATCAAGATGCATCTGAGGGAGAA  1560
Db  1489 ------------------------------------------------------   1488

Qy  1561 GCACCTGTGCAGGACATTGAAAAAGACTTGAAACAAATGAGGCCTTCAGAACAACAAAGGAA  1620
         ||||||||       ||||||||||||||||||||||||||||||||||||||||||||||
Db  1489 --------AGGACATTGAAAAAGACTTGAAACAAATGAGGCCTTCAGAACAACAAAGGAA     1538

Qy  1621 AGTAAAAATCCAGAACAGAGAAATATAAAGCTAAGAAGGGGTAAAATTGAAATTAATTTA  1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1539 AGTAAAAATCCAGAACAGAGAAATATAAAGCTAAGAAGGGGTAAAATTGAAATTAATTTA  1598

Qy  1681 GACAAATGTATTTCTGATGAAAACATCCTCAAGAGAGGAAGAGGCAATGGATATACCCAAAT  1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1599 GACAAATGTATTTCTGATGAAAACATCCTCAAGAGAGGAAGAGGCAATGGATATACCCAAAT  1658

Qy  1741 GAAACTTTGACCTTTGAGGATGCATGAAGTTTAAGGAATATGAATGTGTAAAGGAGCAT  1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1659 GAAACTTTGACCTTTGAGGATGCATGAAGTTTAAGGAATATGAATGTGTAAAGGAGCAT  1718

Qy  1801 GGAGATTATACAGACAAGCAATTTGAAAAACTTCACTGCCCAGAAGCAGGTTTTCCACG  1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||   |||||
Db  1719 GGAGATTATACAGACAAGCAATTTGAAAAACTTCACTGCCCAGAAGCAGCATTTACAGAA  1778

Qy  1861 CAGACT  1866
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Db  1779 CTGACT  1784
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RESULT 5
US-10-730-010-1
; Sequence 1, Application US/10730010
; Publication No. US20040142366A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001212CIPDIV-II
; CURRENT APPLICATION NUMBER: US/10/730,010
; CURRENT FILING DATE: 2003-12-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
US-10-730-010-1
; SEQ ID NO 1
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-730-010-1

Query Match   80.6%; Score 1654; DB 17; Length 2370;
Best Local Similarity   94.5%; Pred. No. 0;
Matches 1763; Conservative 0; Mismatches 10; Indels 93; Gaps 1;

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Qy   1  ATGGATAAGTAAGTACGATGTGATTGATTAAGGCATGGCCAAGGTGCCTTCGGGAAAGCATACTTA   60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  12  ATGGATAAGTAAGTACGATGTGATTGATTAAGGCATGGCCAAGGTGCCTTCGGGAAAGCATACTTA   71

Qy  61  GCTAAAGGGAAATCAGATAGCAAGCACTCTGTCTCAAAGAAAGAAGTCTTCAAAGAAGATGAAATG  120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72  GCTAAAGGGAAATCAGATAGCAAGCACTCTGTCTCAAAGAAAGAAGTCTTCAAAGAAGATGAAATG  131

Qy  121 CCCATACAAGAGAAAAAGAAAGAAGCTTCAAAGAAAGAAAGTGATTCTTCTGAAAAAGATGAAACAT  180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  132 CCCATACAAGAGAAAAAGAAAGAAGCTTCAAAGAAAGAAAGTGATTCTTCTGAAAAAGATGAAACAT  191
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Db   1272 GTGGGAAGCAATTGGGTCTTCGTCCATCTTCTGCCGAGCCAAATTACAACCAGAGACCAA 1331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1321 GAGCTAAGAAGTAGTGAGGAGAGAGCCTAGATTCCAGGAGGACTGCTGCCATTGAGGAAAAACCAA 1380
          ||||||||||||||||||||||
Db   1332 GAGCTAAGAAGTAGTGAGGAGAGAGCCCTAGATTCCAGGAGGACTGCTGCCATTGAGGAAAAACGAA 1391

Qy   1381 ATGAAGGAACAGGAATATTGGAAGCAGTAGAGGAAATACGCCAACAGTACCACCAATGAC 1440
          |||||||||||||||||||||||||||||||||| ||||||||
Db   1392 ATGAAGGAACAGGAATATTGGAAGCAGTAGAGGAAATACGCCAACAGTACCTCCAATGAC 1451

Qy   1441 ATGAAAGAAATTAGAAAAGAAGATGGGGAGGAGGAACCAGAGGAGAACTCAAAAATAAGTCAT 1500
          |||||||||||||||||||||||||||||||||||||||
Db   1452 ATGAAAGAAATTAGAAAAGAAGATGGGGAGGAGAGAACCAGAGGAGAACCAG--------- 1488

Qy   1501 AAAACCTATTTGGTGAAGAGAGTAACCTGCCTGTCCATCAAGATGCATCTGAGGGGAGA 1560
          --------------
Db   1489 ---------------------------------------------------------- 1488

Qy   1561 GCACCTGTGCAGGACATTGAAAAAGACTTGAAACAAAATGAGGCTTCAGAACACAAAGGAA 1620
          ||||||||||| ||||||
Db   1489 --------------AGGACATTGAAAAAGACTTGAAACAAAATGAGGCTTCAGAACACAAAGGAA 1538

Qy   1621 AGTAAAAAATCCAGAACAGAATATAAAGCTAAGAAGTAGTAAGAGGGGTAAAATTAATTTA 1680
          |||||||||||||||||||||||||||||||||||
Db   1539 AGTAAAAAATCCAGAACAGAATATAAAGCTAAGAAGTAGTAAGAGGGGTAAAATTAATTTA 1598

Qy   1681 GACAAATGTATTTCTGATGAAAACATCCTCCAAGAGGAAGAGGCAATGATATACCAAAT 1740
          ||||||||||||||||||||||||||||||||||||||
Db   1599 GACAAATGTATTTCTGATGAAAACATCCTCCAAGAGGAAGAGGCAATGATATACCAAAT 1658

Qy   1741 GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGAATGTGTAAAGGAGCAT 1800
          ||||||||||||||||||||||||||||||||||||||
Db   1659 GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGAATGTGTAAAGGAGCAT 1718

Qy   1801 GGAGATTATACAGACAAAGCCATTTGAAAAACTTCACTGCCCCAGAAGCAGGGTTTTCCACG 1860
          |||||||||||||||||||||||||||||||||||
Db   1719 GGAGATTATACAGACAAAGCCATTTGAAAAACTTCACTGCCCCAGAAGCAGCATTTACAGAA 1778

Qy   1861 CAGACT 1866
          |||||
Db   1779 CTGACT 1784
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RESULT 6
US-10-114-270-187
; Sequence 187, Application US/10114270
; Publication No. US20040030110A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Liu, Ziaohong
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Li, Li
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gorman, Linda
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Ji, Weizhen
; APPLICANT: Anderson, David W.

; APPLICANT: Liete, Mario W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Stone, David J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Rothenberg, Mark E.
; TITLE OF INVENTION: No. US20040030110Alel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-322C
; CURRENT APPLICATION NUMBER: US/10/114,270
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/281,086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 187
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (99)..(1308)
US-10-114-270-187

Query Match   58.0%;   Score 1190.2;   DB 16;   Length 1587;   .
Best Local Similarity   99.5%;   Pred. No. 7;7.8e-309;
Matches 1205;   Conservative   0;   Mismatches   3;   Indels   3;   Gaps   1;

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Qy    1 ATGGATAAGTAACGATGTCGATGTGATTAAGGCCATGCGGCTGCCTTCGGCGGAAGCATACTTA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   99 ATGGATAAGTAACGATGTCGATGTGATTAAGGCCATCGGCTGCCTTCGGCGGAAGCATACTTA 158

Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTTCATAAAGAGATCAATTTGAAAAGATG 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  159 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTTCATAAAGAGATCAATTTGAAAAGATG 218

Qy  121 CCCATACAAGAAAAGAAGAGCTTCAAAGAAGAGTGATTCTTCTGGAAAAGATGAAACAT 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  219 CCCATACAAGAAAAGAAGAGCTTCAAAGAAGAGTGATTCTTCTGGAAAAGATGAAACAT 278

Qy  181 CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAAATGGCAGGCTGTTATTGTAATG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  279 CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAAATGGCAGGCTGTTATTGTAATG 338

Qy  241 GAATATTGTGATGGAGGGATCTCATGAAAAGGATCATAGACAACAACGGGGTGTTATTT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  339 GAATATTGTGATGGAGGGATCTCATGAAAAGGATCATAGACAACAACGGGGTGTTATTT 398

Qy  301 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTACAGACTAAAACATATTCAT 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  399 AGTGAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTACAGACTAAAACATATTCAT 458

Qy  361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  459 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 518
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Qy   421  ATGGTGGCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   519  ATGGTGGCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAGTTCCATGGAACTT  578

Qy   481  GCTCGAACTTGTATTGGAACACCTTACCTACCTGTCCCCAGAGATCTGTCAGAATAAACCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   579  GCTCGAACTTGTATTGGAACACCTTACCTACCTGTCCCCAGAGATCTGTCAGAATAAACCC  638

Qy   541  TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTCTTATATGAGCTCTGCACACTT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   639  TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTGTGTCTTATATGAGCTCTGCACACTT  698

Qy   601  AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACAT  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   699  AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACAT  758

Qy   661  TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   759  TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT  818

Qy   721  CAAGTATCTCCTCGAGACCGACCATCCATAAATTCATTTGAAAAGGCCCTTTTTAGAG  780
          |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db   819  CAAGTATCTCCTCGAGACCGACCATCCATAAATTCATTTGAAAAGGCCCTTTTTAGAG  878

Qy   781  AATCTTATTCCCAAATATTTGACTCCTGAGGTCA---TTCAGGAAGAATTCAGTCACATG  837
          |||||||||||||||||||||||||||||||||     |||||||||||||||||||||
Db   879  AATCTTATTCCCAAATATTTGACTCCTGAGGTCAGTTTGAGGAAGAATTCAGTCACATG  938

Qy   838  CTTATATGCAGAGCAGGAGCGCCAGCTTCTCGACATGCTGGGAAGTGGTCCAGAAGTGT  897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   939  CTTATATGCAGAGCAGGAGCGCCAGCTTCTCGACATGCTGGGAAGGTGGTCCAGAAGTGT  998

Qy   898  AAAATACAAAAGTGAGAGTCAGGGAAAGTGCCCACCAAGATCAAGGATATCTGTGCCA  957
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   999  AAAATACAAAAGTGAGAGTTCAGGGAAAGTGCCCACCAAGATCAAGGATATCTGTGCCA  1058

Qy   958  ATTAAAAGGAATGCTATATTGCATAGAAATGAATGGAGACCCAGCTGGAGCCCCAGAAG  1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1059 ATTAAAAGGAATGCTATATTGCATAGAAATGAATGGAGACCCAGCTGGAGCCCCAGAAG  1118

Qy   1018 GCCAGATCTATAAAAATGATAGAAAAGACCCAAAATTGCTGCTGTCTGTGACATTATGAT  1077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1119 GCCAGATCTATAAAAATGATAGAAAAGACCCAAAATTGCTGCTGTCTGTGACATTATGAT  1178

Qy   1078 TATTATTATGCTCAACTTGATATGCTGAGGAGGAGGAGCCCACAAACCAAGTTATCACCCT  1137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1179 TATTATTATGCTCAACTTGATATGCTGAGGAGGAGGAGCCCACAAACCAAGTTATCACCCC  1238

Qy   1138 ATTCCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCATGGTCCATCC  1197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1239 ATTCCTCAAGAAAATACTGGAGTTGAGGATTACGGTCAGGAAACGAGGCATGGTCCATCC  1298

Qy   1198 CCAAGTCAATG  1208
          |||||||||||
Db   1299 CCAAGTCAATG  1309
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RESULT 7
US-10-114-270-185
; Sequence 185, Application US/10114270
; Publication No. US20040030110A1
GENERAL INFORMATION:

; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Liu, Ziaohong
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Li, Li
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Gorman, Linda
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Ji, Weizhen
; APPLICANT: Anderson, David W.
; APPLICANT: Liete, Mario W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Stone, David J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Rothenberg, Mark E.

; TITLE OF INVENTION: NO. US20040030110A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-322C
; CURRENT APPLICATION NUMBER: US/10/114,270
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/281,086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 185
; LENGTH: 1453
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1198)
US-10-114-270-185

Query Match   57.4%; Score 1178.4; DB 16; Length 1453;
Best Local Similarity 99.2%; Pred. No. 1.1e-305;
Matches 1198; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

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Qy     1  ATGGATAAGTAACGATGTGATTAAGGCTTCGGGAAGGTGCCTTCGGGAAAGCATACTTA  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATGGATAAGTAACGATGTGATTAAGGCCATCGGGAAGGTGCCTTCGGGAAAGCATACTTA  60

Qy    61  GCTAAAGGGAAATCAGATAGCAAGCAACACTGTGTCATAAAAGAGATCAATTTTGAAAGATG  120
          |||||||||||||||| |||||||||| |||||||||||||||||||||||||||| |||
Db    61  GCTAAAGGGAAATCAGATAGCAAGCAACACTGTGTCATAAAAAGAGATCAATTTTGAAAG--  117

Qy   121  CCCATACAAGAAAAAGAAGCTTCAAAGAACAAGAAAGTGATTCTTCTGGAAAAGATGAAACAT  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   118  ------CAAGAAAAAGAAGCTTCAAAGAAAGAAGAAAGTGATTCTTCTGGAAAAGATGAAACAT  171

Qy   181  CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAATGGCAGGCTGTTTATTGTAATG  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   172  CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAATGGCAGGCTGTTTATTGTAATG  231
```

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Query Match        17.9%;   Score 368;   DB 9;   Length 3645;
Best Local Similarity   66.0%;   Pred. No. 1.3e-87;
Matches 549;   Conservative  0;   Mismatches 280;   Indels  3;   Gaps  1;

Qy    1 ATGGATAAGTACGATGTGATTGAAGGCCATCGGGCAAGGTGCCTCGGGAAAGCATACTTA  60
          ||||| ||||| || |   |  || ||   || || |||||    ||| |||||| |||||
Db    1 ATGGAGAAGTATGTTAGACTACAGCAAGAAGATTGGAGAAGGTTCATTTGGAAAAGCCATTCTT  60

Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG 120
          | ||| || |||||  ||| | || || | |||  | ||   | |  | |||||| |||
Db   61 GTTAAATCTACAGAGAGATGGCGAGACAGTATGTTATCAAGGAAATTAACATCTCAAGAAATG 120

Qy  121 CCCATACAAGAAAAAGAAGAGCTTCAAAGAAGAAGAGTGATTCTTCTGGAAAAGATGAAAACAT 180
          ||| | | | ||||| ||||| |   || ||| | || |   |  |  ||| ||| |  |  ||
Db  121 TCCAGTAAAGAAAAGAAGAGCAATCAAGGAGGAGAAGTTGGCAAACATGAAGCAT 180

Qy  181 CCCAACATTGTAGCCTTCTTCAATTCATTCAAGAGAATCATTCAAGAGAAAGATCATGGTTATTGTAATG 240
Db  181 CCAAATATTGTCCAGTATAGAGAATCATTGAAGAGAAAAATGGCTCTCTCACACTAGTAATG 240

Qy  241 GAATATTGTGATGAGGGGATCAATGAAGGATCAATGAGACAACGGGGTGTGTTATT 300
Db  241 GATTACTGTGAGGGAGGGGGGATCGTTTGTTGTACAGATTCTCAGGACTAAAACATATTCAT 300

Qy  301 AGTGAAGATCAGATCAGTGGTTGTGTTGTACAGGGACATATTCTTAGGAACTAAAACATATTCAT 360
Db  301 CAAGAGGATCAGATTTTGACTGGTTTGTACAGATATGTTTGCCCTGAAACACATGTACACAT 360

Qy  361 GACAGGAAGATATTACACAGGGACTAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
Db  361 GACAGGAAGAATTACACGGGACATTTGGAATTGCTGGACATTATTGTGGACACTGAT 420

Qy  421 ATGGTGGCAAAGCTTGGGACTTGGGACTTGGTATAGCAGAAGTCCTGAATAATTCCATGGAACTT 480
Db  421 ATGGTGGCAAAGCTTGGGACTTGGGATTTTGGAGATTTTGGAATTGCTCTAATTCTTTAACTGATGA 477

Qy  481 GCTCGAACTTGTATGGAACACCTGTCCCCAGAGATCTGTCAGAATAAACCC 540
Db  478 ACAGT--ACAACTTGGAGATTTGGAATTGCTCTAGAGTTCTTAGTACTGTTCTTAGAGCTG 537

Qy  541 TACAACAATAAAACCGATATTTGGTCTTCGTGTCTTATATGAGCTCTGCACACTT 600
Db  538 TACAACAATAAAAGTGACATTTGGGTCTCTTTTATGAGAGTTCTTCTGAAGATCT 597

Qy  601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTCGAAGATTTGTCAAGCACAT 660
Db  598 AAACATGCTTTTGAGCTTTGAGAGGTACTGGTACAGCTGCAGTGTAGACTGGACTGAAGATAATATCTGAGATCCT 657

Qy  661 TTTGCCCCAATATCTCCTGTTTCTCGTGAGCTCCATTCCTTCTGATAATCTCAGCTCTTT 720
Db  661 TTTGCCCCAATATCTCCGGGGGTTTTTCGTGAGCTCCATTCCTTCTGAGATCCTTGAGATCT 720
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Db   481  GCTCGAACTTGTATTGGAACAACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCC  540
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  1011  GCTCGAACTTGCATAGGGACCCCATCACTACTTGTCACCTGACCTGTGAAATCTGTGAAACAAACCT 1070

Qy   541  TACAACAATAAAACGGATATTGGTCTTGGCTGTGTCTTATATGAGCTCGCACTT  600
          |||||||||||||||| |||||||||||||||||||||||||| |||||||||
Db  1071  TACAATAATAAAAGTGACATTTGGGCTCTTATGAGCTGTGTACACTT 1130

Qy   601  AAACATCCTTTGAGGGTAACAACTTACACGCAGCTGGTTCTGAGCATTGTCAAGCACAT  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1131  AAACATGCTTTTGAAGCTGGCAGTATGAAAAACCTGTACTGACTGAATATCTGGATCT 1190

Qy   661  TTTGCCCAAATATCTCCGGGGTTTTCTCGTAAGTCCATTCCTTGATATCTCAGCTCTTT  720
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  1191  TTTCACCTGTGTCTTGCATTATTCCTCCGCAGTTTGGTGTCTCAGTTATTT 1250

Qy   721  CAAGTATCTCCTGAGACCGACCATCCATAAATTCCATTTTGAAAAGGCCCTTTTTAGAG  780
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db  1251  AAAAGAAATCCTAGGGATAGACCATCCATTCCAACTCCATATTGGAGAAAAGGTTTTATAGCC 1310

Qy   781  AATCTTATTCCCAAATATTTGACTCCTCTCCTCAGCTTATTGCAGAGAATTCAGTC  832
          ||  ||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  1311  AAACGCATTGAAAAGTTTCTCTCCTCAGCTTATTGCAGAGAATTTTGTC 1362
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RESULT 10
US-10-037-270-246
; Sequence 246, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Liu, Chenghua
;   APPLICANT: Asundi, Vinod
;   APPLICANT: Zhang, Jie
;   APPLICANT: Ren, Feiyan
;   APPLICANT: Chen, Rui-hong
;   APPLICANT: Zhao, Qing A.
;   APPLICANT: Wehrman, Tom
;   APPLICANT: Xue, Aidong J.
;   APPLICANT: Yang, Yonghong
;   APPLICANT: Wang, Jian-Rui
;   APPLICANT: Zhou, Ping
;   APPLICANT: Ma, Yunqing
;   APPLICANT: Wang, Dunrui
;   APPLICANT: Wang, Zhiwei
;   APPLICANT: Tillinghast, John
;   APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
;   FILE REFERENCE: 784CIP2B
;   CURRENT APPLICATION NUMBER: US/10/037,270
;   CURRENT FILING DATE: 2002-01-04
;   PRIOR APPLICATION NUMBER: 09/552,317
;   PRIOR FILING DATE: 2000-04-25
;   PRIOR APPLICATION NUMBER: 09/488,725
;   PRIOR FILING DATE: 2000-01-21
;   NUMBER OF SEQ ID NOS: 1104
;   SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 246
;   LENGTH: 5448
;   TYPE: DNA
;   ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (534)..(4178)
US-10-037-270-246

Query Match   17.9%;   Score 368; DB 15; Length 5448;
Best Local Similarity   66.0%;   Pred. No. 1.7e-87;
Matches 549; Conservative 0; Mismatches 280; Indels 3; Gaps 1;

Qy   1 ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTA 60
          ||||||||||||||||| |||||||||||||||| |||||||| |||||||||||
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```
Db   658  TTTCCACCTGTCGTCTTTGCATTATTCCTATGATCTCCCGCAGTTTGGTGTCTCAGTTATTT  717

Qy   721  CAAGTATCTCCTGAGACCGACCATCCATCCATAAATTCCATTTTGAAAAGGCCCTTTTTAGAGCC  780
          ||   ||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   718  AAAAGAAATCCTAGGGATAGACCACCATCAGTCAACTCCATATTGGAGAAAGGTTTATAGCC  777

Qy   781  AATCTTATTCCCAAATATTTGACTCCTCTCCTCAGCTTATTGCAGAGAATTCAGTC  832
          ||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   778  AAACGCATTGAAAAGTTTCTCTCCTCAGCTTATTGCAGAGAATTTTGTC  829
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RESULT 9
US-09-783-320-50
; Sequence 50, Application US/09783320
; Patent No. US20020038011A1
; GENERAL INFORMATION:
;   APPLICANT: Walke, D. Wade
;   APPLICANT: Hu, Yi
;   APPLICANT: Nepomnichy, Boris
;   APPLICANT: Turner, C. Alexander Jr
;   APPLICANT: Zambrowicz, Brian
; TITLE OF INVENTION: No. US20020038011A1el Human Kinases and Polynucleotides Encoding
; TITLE OF INVENTION:
;   FILE REFERENCE: LEX-0137-USA
;   CURRENT APPLICATION NUMBER: US 60/183,582
;   PRIOR APPLICATION NUMBER: US 60/183,582
;   PRIOR FILING DATE: 2000-02-18
;   PRIOR APPLICATION NUMBER: US 60/184,014
;   PRIOR FILING DATE: 2000-02-22
;   NUMBER OF SEQ ID NOS: 50
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
;   LENGTH: 5426
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-783-320-50

Query Match   17.9%;   Score 368; DB 9; Length 5426;
Best Local Similarity   66.0%;   Pred. No. 1.7e-87;
Matches 549; Conservative 0; Mismatches 280; Indels 3; Gaps 1;

Qy   1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTA 60
          |||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   534 ATGGAGAAGTATGTTAGACTACAGAAGATTGGAGAAGTTCATTGAGAAAGCCATTCTT 593

Qy   61 GCTAAAGGGAAATCAGATAGAGCAAGCACTGTGTCATAAAGAGATCAATTTTGAAAAGATG 120
          || ||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   594 GTTAAATCTACACGAGATGGCGCACAGTATGTTATCAAGGAAATTAACATCTCAAGAATG 653

Qy   121 CCCATACAAGAAAAAGAAGCTTCAAAGAAGAAGTCAAAGAAGATGAAACAT 180
          || ||||||||||||||||||||| ||||||||||||||||||||||||||
Db   654 TCCAGTAAAGAGAAGAGAGAGAATCAAGGAGAAGAGTTGCAGTATGCAAACATGAAGCAT 713

Qy   181 CCCAACATTGTAGCCTTCTTCAATTCATTCATTGTACGGAAGAATGGCAGGCGTGTTTATTGTAATG 240
          || ||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   714 CCAAATATTGTCCAGTATAGAGAAGAATCATTTGAAGAAAAATGGCTCTCCTCTACACTAGTAATG 773

Qy   241 GAATATTGTGATGGAGGGAGATCTCATGAAAAAGGATCAATAGACAACGGGGTGTGTTATTT 300
          ||||| |||||||||| |||||||||||||||||||||||||| ||||||||||||
Db   774 GATTACTGTGAGGGAGGGGATCGTCTGTTTAAGCGAATAAATGCTCAGAAAGGCTTTTGTTT 833

Qy   301 AGTGAAGATCAGATCCTCGGTTGGTTGGTTTGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT 360
          ||||||||||||||||||||||| ||||||||||||||||| |||||||||||
Db   834 CAAGAGGATCAGATTTTGGACTTGGTTTGTACAGATATGTTTGGCCCTGAAACATGTACAT 893

Qy   361 GACAGGAAGAATATTACACAGGGACATAAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
          ||||| ||||||||||| |||||||||||||||||||||||| |||||
Db   894 GATTAGAAAAAATTCCTCATCGAGACATTAAATCTCAGACAAATTTTTAACTAAAGATGGA 953

Qy   421 ATGGTGGCAAAGCTTGGGGACTTGGGATAGCAAGAGTCCTGAATAATTCCATGGAACTT 480
          |||| |||||||||||||||| |||||| ||||||| |||||||||| |||||||
Db   954 ACAGT--ACAACTTGGAGATTTTGGAGATTTGGAATTGCTAGAGTTCTTAATAGTACTGTAGAGCTG 1010
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 ;  PRIOR FILING DATE: 2000-04-25
 ;  PRIOR APPLICATION NUMBER: 09/488,725
 ;  PRIOR FILING DATE: 2000-01-21
 ;  NUMBER OF SEQ ID NOS: 1104
 ;  SOFTWARE: pt_FL_genes Version 1.0
 ;  SEQ ID NO 246
 ;  LENGTH: 5448
 ;  TYPE: DNA
 ;  ORGANISM: Homo sapiens
 ;  FEATURE:
 ;  NAME/KEY: CDS
 ;  LOCATION: (534)..(4178)
 ;  US-10-117-722-246

Query Match        17.9%;    Score 368;  DB 15;  Length 5448;
Best Local Similarity    66.0%;    Pred. No. 1.7e-87;
Matches  549;    Conservative  0;  Mismatches  280;  Indels  3;  Gaps  1;

Qy        1 ATGGATAAGCTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTCGGGAAGCATACTTA   60
            |||||||| ||| |  |||||   ||||||||  ||| |||||  | |||||||
Db      534 ATGGAGAAGAAGTATGTTAGACTACAGAAGATTGGAGAAGGTTCATTGGGAAAAGCCATTCTT  593

Qy       61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAGAGATCAATTTGAAAAGATG  120
            |||||    ||||| |||  |||||| |||   ||||||||| |  ||| ||||
Db      594 GTTAAATCTACAGAGATGGCAGACAGTATGTTATCAAGGAAATTAACATCTCAAGAATG  653

Qy      121 CCCATACAAGAAAAAGAAGCTTCAAAGAAAGAAGTGATTCTTCTGGAAAAGATGAAACAT  180
            |||| |||||||| ||||| |  ||| ||| |||   |||  ||||||||
Db      654 TCCAGTAAAGAAAGAAGAGAGAATCAAGGAGAAGTTGCAGTATTGGCAAACATGAAGCAT  713

Qy      181 CCCAACATTGTAGCCTTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATTT  240
            ||||  |||||   ||  |   ||| ||||| | |||||| | |||| |||||
Db      714 CCAAATATTGTCCAGTATGCTAGAGAATGGCAAGCTGCTCCTCTACAGTAATG  773

Qy      241 GAATATTGTGATGGAGGGGATCCATGAAAAGGATCAATAGACTAAAACATATTCAT  300
            ||| ||| | || || |||||  | | ||| ||||   |  ||| ||||| |
Db      774 GATTACTGTGGAGGGGAGGGGATCGTTGACTGTTGTACAGATTTGTACACATGTACAT  833

Qy      301 AGTGAAGATCAGATCCTCGGTGGTTGTGTACAGATTTCTCTAGGACTAAAACATATTCAT  360
            |||||| || |||| ||| || || ||||| |||||||| ||||| |||||
Db      834 CAAGAGGATCAGATTTTGGAAGCTGGGACTGGTTGCAGATATGTTTGGCCCTGAAACATGTACAT  893

Qy      361 GACAGGAAGATATTACACAGGGACTCAGAACATTTTCTTAGCAAGAACGGA  420
            || ||||| ||| | || ||||| |  ||||  ||  ||||| | | |
Db      894 GATAGAAAATTCTTCATCGAGACATTAAATCTCAGAACATTTTTAACTAAAGATGA  953

Qy      421 ATGGTGGCAAAGCTTGGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480
            |||||||||||| || ||||| |||||  | |||||   |||||||||| |||||
Db      954 ACAGT---ACAACTTGGAGATTTGGAATTGCTAGAGTTCTTAATACTGTGAGAGCTG  1010

Qy      481 GCTCGAACTTGTATTGACACCTTACTACCTGTCCCCAGAGATCGTGTCAGAATAAACCC  540
            |||||||| |||| |  |   |  ||| |||   ||| ||| | |  |||||||
Db     1011 GCTCGAACTTGCATTAGGGACCCCCATACTCTGTCACCTGAAATCGTGAAAACAAACCT  1070

Qy      541 TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTCGGGGGTGTCTTTATGAGCTCTCCACACTT  600
            |||| ||||  ||  |||||||||||  ||||| |||||| |||||  || | ||| |||||
Db     1071 TACAATAATAAAAGTAGACATTTGGCCTCGGGGGTGTGTCTTTTATGAGCTGTGTCACATT  1130

Qy      601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACAT  660
            |||||| ||||||||  ||  |    | | |  |  |  ||||||  | |  ||| |
Db     1131 AAACATGCTTTTGAAGCTGGCAGTATGAAAAACCTGGTACTGAAGATAATATCTGGATCT  1190

Qy      661 TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTGAGCTCTTT  720
            ||| |   || |  || || |||||| | ||    |   || |||  |||
Db     1191 TTTCCACCTGTCTTGCATTATTCCTATGATCCTCCTATGATCTCCATGATCTCCAGTTATT  1250

Qy      721 CAAGTATCTCCTGAGACCGACCATCCATAAATTCCATTTGAAAAGGCCCTTTTTAGAG  780
            |||| ||||| ||| || | |    ||   | || |||||||| |  || |||||
Db     1251 AAAAGAAATCCTAGGATAGACCATCAGTCAACTCCATATTGGAGAAAGGTTTTATAGCC  1310

Qy      781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAGAATTCAGTC  832
            || |||| ||  |||| ||||||| ||  | |||||| ||||||| |  |
Db     1311 AAACGCATTGAAAAGTTTCTCTCCTCAGCTTATTGGAGAAGAATTTGTC  1362
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RESULT 11
US-10-117-722-246
; Sequence 246, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zharg, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1e1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2BCIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317

```
Db    894  GATAGAAAATCTTCATCGAGACATTAAATCTCAGAACATATTTTAACTAAAGATGGA  953
           ||||| |||||||||||||||||||||||||||||||||||||||| ||||||||||
Qy    421  ATGGTCGCAAAGCTTCGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480
           ||| |||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    954  ACAGT---ACAACTTGGAGATTTGGAATTGCTAGAGTTCTTAATAGTACTGTAGAGCTG  1010

Qy    481  GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCTGTCAGAATAAACCC  540
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   1011  GCTCGAACTTGCATAGGGACCCCACATACTACTTGTCCACCTGAAATCTGTGAAACAAACCT  1070

Qy    541  TACAACAATAAACCGATATTGGTCTCTTGGCTGTGTCTTTATATGAGCTCTGCACACTT  600
           ||||| |||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1071  TACAATAATAAAAGTGACATTTGGGCTCTGGGGTGTGTCCTTATGAGCTGTGTACACTT  1130

Qy    601  AAACACCCTTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTGTCAGCACACAT  660
           ||| |||||||||||||||||||| || ||||||||||||||||||||||||||  |||||
Db   1131  AAACATGCTTTTGAGGCTGGCAGTATGAAAAAACCTGGTACTGACGATATAATCTGGATCT  1190

Qy    661  TTTGCCCAATATCTCCGGGGGTTTTCTGTGAGCTCCATTCCTTGATATCTCAGCTCTTT  720
           ||| ||||||||||| || |||||||||| ||||||||||||||||||||||||||  |||
Db   1191  TTTCCACCTGTCTTTGCATTATTCCTATGATCTCCGCAGTTTGGTGTCTCAGTTATTT  1250

Qy    721  CAAGTATCTCCTCGAGACGACCGACCATCCATCCATAAATTCCATTTGAAAGGCCCTTTTAGAG  780
           |||||||| | || ||||||||| || |||||| |||||||||||||||||||| |||| |||
Db   1251  AAAGAAATCCTAGGATAGACCTAGCCATCCAACTCCATATTGGAGAAAGTTTTATAGCC  1310

Qy    781  AATCTTATTCCCAAATATTTGACTCCTGAGTCATTCAGGAAGAATTCAGTC  832
           ||| ||||| || || ||||||||||||||||||||||||| ||||| |||
Db   1311  AAACGCATTGAAAAGTTTCTCTCTCCTCAGCTTATTGCAGAAGAATTTGTC  1362
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RESULT 12
US-10-037-270-245
; Sequence 245, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Liu, Chenghua
;   APPLICANT: Asundi, Vinod
;   APPLICANT: Zhang, Jie
;   APPLICANT: Ren, Feiyan
;   APPLICANT: Chen, Rui-hong
;   APPLICANT: Zhao, Qing A.
;   APPLICANT: Wehrman, Tom
;   APPLICANT: Xue, Aidong J.
;   APPLICANT: Yang, Yonghong
;   APPLICANT: Wang, Jian-Rui
;   APPLICANT: Zhou, Ping
;   APPLICANT: Ma, Yunqing
;   APPLICANT: Wang, Dunrui
;   APPLICANT: Wang, Zhiwei
;   APPLICANT: Tillinghast, John
;   APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US2003010452941el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 245
;   LENGTH: 5532
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (534)..(4262)
US-10-037-270-245

Query Match   17.9%;   Score 368;   DB 15;   Length 5532;
Best Local Similarity   66.0%;   Pred. No. 1.7e-87;
Matches   549;   Conservative   0;   Mismatches   280;   Indels   3;   Gaps   1;

```
Qy      1  ATGGATAAGTACGATGTGATTAAGGCCATCGGGCGTGCCTTCGGGAAAGCATACTTA  60
           |||||||||| | ||||||||| | ||||||| ||||||||||||||||| |||||||
Db    534  ATGGAGAAGTATGTTAGACTACAGAAGAAGATTGGAGAAGATTGGAAAAGCCATTCTT  593

Qy     61  GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG  120
           ||| | |||||||| |||| | || |||||||| |||| ||||| || ||||||||||
Db    594  GTTAAATCTACAGAAGATGGCAGACAGTATGTTATCAAGGAAATTAACATCTCAAGAAATG  653

Qy    121  CCCATACAAGAAAAAAGAAGCTTCAAAGAAGAGCTTCAAAGAAGAGTGATTCTTCTGGAAAAGATGAAACAT  180
           ||||| ||||| || |||||||  |  | |||| | | ||| | ||||||||||||||| |||
Db    654  TCCAGTAAAGAAAGAGCAGAGAGAATCAAGGAGAGAAGTTGCAGTATTGGCAAACATGAAGCAT  713

Qy    181  CCCAACATTGTAGCCCTTCTTCCAATTCATTTCATTTCAAGAGAATGGCAGGCTGTTTATTGTAATG  240
           ||||| | || | ||  |||| ||| |||| ||  |||||| || |||||||| | |||
Db    714  CCAAATATTGTCCAGTATAGAGAATCAATTCATTTGAGAGAAAATGGCTCTCTACATAGTAATG  773

Qy    241  GAATATTGTGATGGTGAGGGATCCATGAAAGGATCCATGAAAGAAAAGGATCAATAGACAACGGGGTGTGTTATTT  300
           || | |||| |||| || || || | ||| ||| |||  ||||||| || ||| ||| | |||||||
Db    774  GATTACTGTGAGGGAGGGATCCGTTTAAGCTGTTTAAGCCGAATAAAATGCTCAGAAAAGGCGTTTTGTTTT  833

Qy    301  AGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTTCTCTAGGACTAAAACATATTCAT  360
           || || |||||| | || |||| | ||||| || |||| |||| |||||| |||| |||
Db    834  CAAGAGGATCAGATTTTGGACTGGTTTGTACAGATATGTTTGGACCCCTGAAACATGTACAT  893

Qy    361  GACAGGAAGAAGATATTACACAGGGACATAAAAGCTCAGAGACAGTTTTCTTAGCAAGAAGATG  420
           |||| |||| | | ||| || || ||| |||||||||||||| | |||||||||| |||||||
Db    893  ATGGAAGATATGTTAGACTACAGAAGAAGATTGGAGAAGATTCATTTGAAAAGCCATTCTT  593
```

RESULT 13
US-10-117-722-245
; Sequence 245, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Liu, Chenghua
;   APPLICANT: Asundi, Vinod
;   APPLICANT: Zhang, Jie
;   APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2BCIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 245
;   LENGTH: 5532
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (534)..(4262)
US-10-117-722-245

Query Match   17.9%;   Score 368;   DB 15;   Length 5532;
Best Local Similarity   66.0%;   Pred. No. 1.7e-87;
Matches   549;   Conservative   0;   Mismatches   280;   Indels   3;   Gaps   1;

```
Qy      1  ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGGCGTGCCTTCGGGAAAGCATACTTA  60
           |||||||||| | ||||||||| | ||||||| ||||||||||||||||| |||||||
Db    534  ATGGAGAAGTATGTTAGACTACAGAAGAAGATTGGAGAAGATTCATTTGAAAAGCCATTCTT  593

Qy     61  GCTAAAGGGAAATCAGATCAGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTGAAAAGATG  120
```

```
Db   594  GTTAAATCTACAGAAGATGGCAGACAGTATGTTATCAAGGAAATTAACATCTCAAGAGATG  653
          |||||   ||||||   ||||   ||||  || |||   |||
Qy   121  CCCATACAGAAAAAGAAGAGCTTCAAGAGAAGAAGAGCTTGATTCTTCTGGAAAAGATGAAACAT  180

Db   654  TCCAGTAAAGAAAGAGAAGAAGAATCAAGGAGAGAAGTTGCAGTAATTGGCAAACATGAAGCAT  713

Qy   181  CCCAACATTGTAGCCTTCTTCCTTCAATTCATTCAGAGAATGGCAGGCTGTTATTGTAATG  240

Db   714  CCAAATAATTGTCCAGTATAGAGAATCATTTGAAGAAAAAGGCTCTCTCACATAGTAATG  773

Qy   241  GAATATTGTGATGGAGGGGGATCCATGAGAAAGGATCAATGAGAAAACGGGGTGTGTTATTT  300

Db   834  CAAGAGGATCAGATTTTGGACTGGTTTGGTTGTACAGATATGTTGGCCCTGAAACATGTACAT  893

Qy   361  GACAGGAAGATATTACACAGAGGGACATAAAAGCTCAGAACATTTTCTTAGCAGAACGGA  420

Db   894  GATAGAAAAATTCTTCATCGAGACATTAAATCTCAGAACATATTTTTAACTAAGATGGA  953

Qy   421  ATGGTGGCAAAGCTTGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT  480

Db   954  ACAGT---ACAACTTGGAGATTTTGGAATTGCTAGAGTTCTTAATAGTACTGTGAGAGCTG  1010

Qy   481  GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCGTTCAGAATAAACCC  540

Db   1011 GCTCGAACTTGCATAGGGACCCCCATACTACTTGTGCACCTGAAATCTGTGAAAACAAACCT  1070

Qy   541  TACAACAATAAAAACGGATATTGTCTTCTTTGGCTGTGTCTTATATGAGCTCTGCACACTT  600

Db   1071 TACAATAATAAAAGTGACATTTGGGCTCTCGGGTGTGTCTTTATGAGCTGTGTACACTT  1130

Qy   601  AAACATCCTTTTGAGGGTAACACTTACAGCAGTGGTTCTGAAGATTTGTCAGCACAT  660

Db   1131 AAACATGCTTTTGAAGCTGGCTGGCAGTGATGAGAAAAACCTGGTACTGGAGATAATATCTGGATCT  1190

Qy   661  TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTGAATATCTCCAGCTCTTT  720

Db   1191 TTTCCACCTGTGTCTTTGCATTATTCCTATGATCTCCGCAGTTTGGTGTCTCCAGTTATTT  1250

Qy   721  CAAGTATCTCCTCCGAGACCGACCATCCATCCATAAATTCCATTTTGAAAAGGCCCTTTTTAGAG  780

Db   1251 AAAAGAAAATCCTAGGGGATAGAACCATCAGTCAACTCAGTGAATAAGGTTTTATAGCC  1310

Qy   781  AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGAATTCAGTC  832

Db   1311 AAACGGCATTGAAAAGTTTCTCTCTCCTCCAGCTTATTGCGAAGAAGAATTTGTC  1362
```

; APPLICANT: Gerlach, Valerie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Ji, Weizhen
; APPLICANT: Anderson, David W.
; APPLICANT: Liete, Mario W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Stone, David J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Rothenberg, Mark E.

; TITLE OF INVENTION: No. US2004003011OA1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-322C
; CURRENT APPLICATION NUMBER: US/10/114,270
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/281,086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 183
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (246)..(1521)
US-10-114-270-183

Query Match   12.7%;   Score 260.8;   DB 16;   Length 1588;
Best Local Similarity   59.0%;   Pred. No. 5.3e-59;
Matches 486;   Conservative   0;   Mismatches 332;   Indels   6;   Gaps   2;

```
Qy     1  ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGCAAGGTGCCTTCGGGAAGCATACTTA  60
          ||||||  ||| || |||||  ||  |||||||||||||  |||| ||
Db   246  ATGGATGACTACATGTGTCCTGAGAATGATTGGGGAGGCCTCTTGCGGCGGAGCTCTTTTG  305

Qy    61  GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGAGATCAATTTTGAAAAGAATG  120
          ||||| || || | |||||  ||||   || |||| |||  |||| |||  |||||||
Db   306  GTTCAGCATGAAAGCAGCAGTAATCAGATACAGATGTTTGCCATGAAAGAATAAGGCTTCCCAAGGTC  365

Qy   121  CCCATACAAGAAAAAGAAGAGCTTCAAAGAAGAAGAGTGATTCTTCTGGAAAAGATGAAACAT  180
          |||| ||||| ||||||||||||||  | ||||||  ||| ||||  |||||  ||||  ||
Db   366  ACTACTAATACACAGAA---TTCTAGGAAGAAGCAGAA---TTCTAGGAAGGATGCAAATGAAACAC  422

Qy   181  CCCAACATTGTAGCCTTCTTCCTTCAATTCATTCAGAGAATGGCAGGCTGTTATTGTAATG  240
          |||| ||||| ||| ||||  || ||  |||| || ||||  ||||  ||| || ||||
Db   423  CCTAATATTGTTGCCTTCAAAGAATCATTTGAAGCTGAAGGACACTTGTATATTGTGATG  482

Qy   241  GAATATTGTGATGGAGGGGGATCCATGAGAAAGGATCAATGAGAAAACGGGGTGTGTTATTT  300
          |||| |||| ||||||| ||| | | ||| ||||||  ||||||  |||||||||||||||
Db   483  GAATACTGTGATGGAGGGGGATCTAATGCAAAGATTAAACAGCAGAAAGAAGGAAAGTTATTT  542
```

RESULT 14
US-10-114-270-183
; Sequence 183, Application US/10114270
; Publication No. US2004003011OA1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Liu, Ziachong
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Li, Li
; APPLICANT: Vernet, Corine
; APPLICANT: Zezhusen, Bryan D.
; APPLICANT: Gorman, Linda
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Burgess, Catherine E.

FILE REFERENCE: 21402-322C
CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR APPLICATION FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,930
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,512
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILING DATE: 2001-04-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SEQ ID NO 181
LENGTH: 1781
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (246)..(1713)
US-10-114-270-181

Query Match   12.6%; Score 259.2; DB 16; Length 1781;
Best Local Similarity 58.9%; Pred. No. 1.5e-58;
Matches 485; Conservative 0; Mismatches 333; Indels 6; Gaps 2;

```
Qy    1 ATGGATAAGTACGATGTGATTGATTAAGGCCATCGGGCAAGTGCCTCGGGAAAGCATACTTA  60
          ||||||   ||  |||  ||| ||  ||| ||  |||| | |||||||||| | |||  ||
Db  246 ATGGATGACTACACATGGTCCTGAGAATGATTGGGGAGGGGCTCCTCGGCAGAGCTCTTTTG 305

Qy   61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATAAAAGATCAATTTGAAAAGATG      120
          |   |   |||   ||||| |  ||  | ||  || |  ||| ||| |||  ||| ||
Db  306 GTTCAGCATGAAAGCAGTAATCAGATGTTTGCCATGAAAGAAGAAGTGAAAATAAGGCTTCCCAAGGTC 365

Qy  121 CCCATACAGAAAAAGAAGCTTCAAAGAAGAAGTGATTCTTCTGGAAAAGATGAAACAT     180
          |  ||  |||||  | |  ||| |||| |||| ||| | ||| |||||  |||||||
Db  366 ACTACTAATACACAGAA---TTCTAGGAAGGAGGAGCTGTGTTCTTTTAGCCAAAATGAAACAC 422

Qy  181 CCCAACATGTGTAGCCTTCTTCAATTCATTTCAAGAGAATGGCAGGCTGCTGTTAATTGTAATG 240
          || || | |||| ||||  |||||| ||||| |||| |   |  | |||  |  || ||| ||
Db  423 CCTAATATTGTTGCCTTCAAAGAATCATTTGAAGCTGAAGGACACTTGTATATTGTGATG      482

Qy  241 GAATATTGTGATGGAGGGGATCTCATGAAAAGGATCAATAGACAACGGGGGTGTGTTATTT    300
          |||||  |||||||||||||| |  |||  ||| | ||| |||| || ||    | |||||
Db  483 GAATACTGTGATGGAGGGGATCTAATGCAAAAGATTAAACAGCAGAAGAAGTTATTT       542

Qy  301 AGTGAAGATCAGATCCTCGGTGGTTTGTACAGACTAAAACATATTCAT               360
          ||||||||||||||   || | ||| | ||||| |||||||||||||
Db  543 CCTGAAGACCAGATACTTAATTGGTTTACCCAAATGTGCCTTGGAGTAAATCACATTCAC  602

Qy  361 GACAGGAAGAGATATTACACAGGGACATAAAAGCTCAGAACATTTTTCTTAGCAAGAACGGA  420
          |||||||||||||||||| || ||||||||||| |||||| || ||| ||||||||||||||
Db  603 AAGAAACGTGTGCTACACAGAGATATCAAGTCCCAGAATATCTTCCTCACTCAGAATGGA   662

Qy  421 ATGGTGGCAAAGCTTGGGGACTTGGTATAGCAAGAGTCCTGAATAATTCCATGGAACTT     480
          | || |  ||| ||||| |||||||    |||||||  | || | | |   | |  |||
Db  663 AAAGTG---AAATTGGGAGACTTTGGATCTGCCCGTCCCGTCTGCGGTTCTCTCCAATCCGATGGCATTT 719

Qy  481 GCTCGAACTTGTATTGGAACACCTTACTACCTGTCCCCAGAGATCGTCAAGAATAAACC    540
          |||||||||||| |||||||||||||||||||| | || ||||||||||||| || ||
Db  720 GCTTGTGAACTTGTATTGGAACTCCTTATTATGTGCCCAGAGATCGTCAAGGATGGGTGC   779

Qy  541 TACAACAATAAAACGGATATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACTT    600
          ||| ||||| |||||||| ||| |||| |||||  ||  |  |||| |||| ||| ||||
Db  780 TATAACAATAAAAGTGACATCTGGTTCCTGGTTGCATCCTGTGATCCTGTATGAACTCTGTACCCTT 839

Qy  601 AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACAT    660
          |||||||| || || | ||||| |||||||||| |||||||||||||| | ||||||||
Db  840 AAGCATCCATTTCAGGGTCAAAATAGTTGGAAAAATCTTATCCTCAAAGTATGTCAAGGTGC 899

Qy  661 TTTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCCATTCCTTGATATCTCCAGCTCTTT 720
          |||||||||||||| |||| |||||| |||||||| |||||| || ||| |||||| || |
Db  900 ATCAGTCCACTGCCGTCTCCATTACTCCTATGAACTTCCAGTTCCTAGTCCTAGCAAGCAGATGTTT 959

Qy  721 CAAGTATCTCCGAGACCGACCACCATCCATAAATTCCATTTTGAAAAGGCCCTTTTTAGAG  780
          |||||||||||  ||||  ||  ||||||  |||||||  |||||||| | | ||| ||||
Db  960 AAAAGGAATCCCTCACATCGCCCTCGCCCTCGGCTACACGGCCGTTCTCTCTCGGGCATCGTAGCT 1019

Qy  781 AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGA               824
          |||||||| |||||  ||||  ||||| | |||||||||||||
Db 1020 CGGCTTGTCCAGAGAGTGCTTACCCCCCGAGATCATCATGGAATA              1063
```

RESULT 15
US-10-114-270-181
Sequence 181, Application US/10114270
Publication No. US20040030110A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
APPLICANT: Liu, Ziaohong
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Li, Li
APPLICANT: Vernet, Corine
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Gorman, Linda
APPLICANT: Shenoy, Suresh G.
APPLICANT: Pena, Carol E.A.
APPLICANT: Smithson, Glennda
APPLICANT: Burgess, Catherine E.
APPLICANT: Gerlach, Valerie
APPLICANT: Padigaru, Muralidhara
APPLICANT: Shimkets, Richard A.
APPLICANT: Gangolli, Esha A.
APPLICANT: Taupier Jr. Raymond J.
APPLICANT: Casman, Stacie J.
APPLICANT: Ji, Weizhen
APPLICANT: Anderson, David W.
APPLICANT: Liete, Mario W.
APPLICANT: Rastelli, Luca
APPLICANT: Edinger, Shiomit R.
APPLICANT: Stone, David J.
APPLICANT: MacDougall, John R.
APPLICANT: Rothenberg, Mark E.
TITLE OF INVENTION: NO. US2004003011OA1e1 Proteins and Nucleic Acids Encoding Same

```
Qy    541  TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT  600
                ||||||||||| || || | ||||||  |||| | |  ||| ||||| || |||
Db    780  TATAACAATAAAAGTGACATCTGGTCCTTGGGTTGCATCCTGTATGAACTCTGTACCCTT  839

Qy    601  AAACATCCTTTGAGGGTAACAACTTACAGCAGCTGGTTCTGAAGATTTGTCAAGCACAT  660
                ||||||||| ||| | || | || |  || |  | ||||| |  |||||||
Db    840  AAGCATCCATTTCAGGCAAATAGTTGGAAAAATCTTATCCTCAAAGTATGTCAAGGGTGC  899

Qy    661  TTTGCCCAATATCTCCGGGGTTTTCTGGTGAGCTCCATTCCTTGATATCTCAGCTCTTT  720
                || |||  | |  ||   ||| |  |    |||  ||| | |||| |||
Db    900  ATCAGTCCACTGCCGTCTCATTACTCCTATGAACTTCAGTTCCTAGTCAAGCAGATGTTT  959

Qy    721  CAAGTATCTCCTGAGACCGACCATCCATAAATTCATTTTGAAAAGGCCCTTTTTAGAG  780
                || |||| |||| |  | |  || |||||   |    |
Db    960  AAAAGGAATCCCTACATCGGCCCTCGGCTACAACGCTTCTCTCGAGGCATCGTAGCT  1019

Qy    781  AATCTTATTCCCAAATATTTGACTCCTGAGGTCATTCAGGAAGA  824
                || ||| ||| | ||  | || |
Db    1020 CGGCTTGTCCAGAAGTGCTTACCCCCGAGATCATCATGGAATA  1063
```

Search completed: October 10, 2004, 15:01:49
Job time : 1354 secs